

[illegible][illegible]

OY		361	GTGGGTAAATTGGAATCCCGAGATGTCATCGGATGTTTTCTTTCAATGATTTGT	420
Dd		361	GTGGGTAAATTGGAATCCCGAGATGTCATCGGATGTTTTCTTTCAATGATTTGT	420
OY		421	GACAAATGCAGCCTCGTGGAGACTTTTTTGTA	454
Dd		421	GACAAATGCAGCCTCGTGGAGACTTTTTTGTA	454
<hr/>				
RESULT 4				
LOCUS	A94725	1565 bp	DNA	linear
DEFINITION	Sequence 3 from Patent WO9334005.			PAT 26-JAN-2000
ACCESSION	A94725			
VERSION	A94725.1	GI:6778990		
KEYWORDS				
SOURCE	unidentified			
ORGANISM	unclassified			
REFERENCE	1 (bases 1 to 1565)			
AUTHORS	DeRose,R. and Freysassin,G.			
TITLE	MAIZE H3c4 PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON,			
JOURNAL	CHIMERIC GENE CONTAINING IT AND TRANSFORMED PLANT			
	Patent: WO 9334005-A 3 08-Jul-1999;			
FEATURES	RHONE POLIENC AGROCHIMIE (FR)			
source	Location/Qualifiers			
	1..1565			
	/organism="unidentified"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:32644"			
promoter	27..1047			
intron	1102..1555			
<hr/>				
Query Match	100.0%; Score 454; DB 6; Length 1565;			
Best Local Similarity	100.0%; Pred. No. 1e-107;			
Matches 454; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
OY	1	GTAAACACCCGCCCTCTCCTCTTCTTCTTCGTTTTTTTTTTCGTCGATCTCAT	60	
Dd	1102	GTAAACACCCGCCCTCTCCTCTTCTTCTTCGTTTTTTTTTTCGTCGATCTCAT	1161	
OY	61	CTTTGGCCTTGGTAGTTGGGTGGGCGAAGCGGCTTGTGCCCAATCGGTGCGCGG	120	
Dd	1162	CTTTGGCCTTGGTAGTTGGGTGGGCGAAGCGGCTTGTGCCCAATCGGTGCGCGG	1221	
OY	121	AGGGCGGGGATCTCGCGGCTGCGCTCCGGGCGTGAATCGGGCCCGATCCMCGCGGGG	180	
Dd	1222	AGGGCGGGGATCTCGCGGCTGCGCTCCGGGCGTGAATCGGGCCCGATCCMCGCGGGG	1281	
OY	181	ATGGGCTCTCGGATGTAGATCTGATCCGCGGTGTTGGGGAGATGATGGGGCGTTAA	240	
Dd	1282	ATGGGCTCTCGGATGTAGATCTGATCCGCGGTGTTGGGGAGATGATGGGGCGTTAA	1341	
OY	241	AATTCGCGATCTAAACAAGATCAGAAGAGGGGAAAAGGCACTATGTTTATATTTT	300	
Dd	1342	AATTCGCGATCTAAACAAGATCAGAAGAGGGGAAAAGGCACTATGTTTATATTTT	1401	
OY	301	TATATATTTTCGCTGCTGCTGTCAGGCTTATAGATGCTTATATCTTTCTTTT	360	
Dd	1402	TATATATTTTCGCTGCTGCTGTCAGGCTTATAGATGCTTATATCTTTCTTTT	1461	
OY	361	GTGGGTAAATTGGAATCCCGAGATGTCATCGGATGTTTTCTTTCAATGATTTGT	420	
Dd	1462	GTGGGTAAATTGGAATCCCGAGATGTCATCGGATGTTTTCTTTCAATGATTTGT	1521	
OY	421	GACAAATGCAGCCTCGTGGAGACTTTTTTGTA	454	
Dd	1522	GACAAATGCAGCCTCGTGGAGACTTTTTTGTA	1555	
<hr/>				
RESULT 5				
AR559745				

LOCUS	ARS59745	1565 bp	DNA	linear	PAT 08-Oct-2004
DEFINITION	Sequence 3 from patent US 6750378.				
ACCESSION	ARS59745				
VERSION	ARS59745.1	GI:53969843			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1565)				
TITLE	DeRose,R. and Freysinet,G. Maize H3c4 promoter combined with the first intron of rice actin, chimeric gene comprising it and transformed plant Patent: US 6750378-A 3 15-JUN-2004;				
JOURNAL	Location/Qualifiers				
FEATURES	1..1565				
source	/organism="unknown" /mol_type="genomic DNA"				
ORIGIN					
Query Match	100.0%;	Score 454;	DB 6;	Length 1565;	
Best Local Similarity	100.0%;	Pred. No.1e-107;			
Matches 454; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
OY	1	GTAACACCCCGCCCTCCTCCTTTTCCTTCCGTTTTTTTTCGTCCGCTGCAT	60		
Db	1102	GTAACACCCCGCCCTCCTCCTTTTCCTTCCGTTTTTTTTCGTCCGCTGCAT	1161		
OY	61	CTTTGGCCTTGTAAGTTGGGTGGGCGAAGACGGCTTCGTGCCAGATCGGTGCGGG	120		
Db	1162	CTTTGGCCTTGTAAGTTGGGTGGGCGAAGACGGCTTCGTGCCAGATCGGTGCGGG	1221		
OY	121	AGGGGCGGGATCTCGCGGCTGCGCTTCGCCGGCTGAGTGGCCCCGATCTCGCGGGGA	180		
Db	1222	AGGGGCGGGATCTCGCGGCTGCGCTTCGCCGGCTGAGTGGCCCCGATCTCGCGGGGA	1281		
OY	181	ATGGGGCTCTCCGATGTAGATCTGATCCGCGTGTGGGGGAGATGATGGGGCGTTAA	240		
Db	1282	ATGGGGCTCTCCGATGTAGATCTGATCCGCGTGTGGGGGAGATGATGGGGCGTTAA	1341		
OY	241	AATTTCGCATGTCAAAACAAGATCAGAGAAGGGGAAAAGGGCACTATGTTTATATTT	300		
Db	1342	AATTTCGCATGTCAAAACAAGATCAGAGAAGGGGAAAAGGGCACTATGTTTATATTT	1401		
OY	301	TATAATTTCTGCTGCTGCTGCTGCAGGCTTAGATGTGCTAGATCTTTCTTTCTTTT	360		
Db	1402	TATAATTTCTGCTGCTGCTGCTGCAGGCTTAGATGTGCTAGATCTTTCTTTCTTTT	1461		
OY	361	GTTGGTGAATTTTAAATCCCTCACACTGTTTCATCGGTAGTTTTCTTTTCAGATTTGT	420		
Db	1462	GTTGGTGAATTTTAAATCCCTCACACTGTTTCATCGGTAGTTTTCTTTTCAGATTTGT	1521		
OY	421	GACAAATGCAGCCTCGTGGCGAGCTTTTGTAG	454		
Db	1522	GACAAATGCAGCCTCGTGGCGAGCTTTTGTAG	1555		
RESULT 6					
BD128391	1565 bp	DNA	linear	PAT 18-SEP-2002	
LOCUS	BD128391				
DEFINITION	Corn H3C4 promoter bonded to the first intron of rice actin, chimeric gene containing this promoter and transgenic plant.				
ACCESSION	BD128391				
VERSION	BD128391.1	GI:23223336			
KEYWORDS	JP 2002500016-A/3.				
SOURCE	unidentified				
ORGANISM	unidentified				
REFERENCE	unclassified.				
AUTHORS	1 (bases 1 to 1565)				
TITLE	DuRose,R. and Freysinet,G. Corn H3C4 promoter bonded to the first intron of rice actin, chimeric gene comprising this promoter and transgenic plant Patent: JP 2002500016-A 3 08-JAN-2002;				
JOURNAL	AVANTIS CROPS SCIENCE SA				

[illegible][illegible]

DEFINITION	O. sativa Act1 gene.
ACCESSION	X63830
VERSION	X63830.1 GI:468505
KEYWORDS	act1 gene; actin; Gus gene.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE	1 McElroy,D., Blowers,A.D., Jones,B. and Wu,R. Construction of expression vectors based on the rice actin 1 (Act1 5', region for use in monocot transformation Mol. Gen. Genet. 231 (1), 150-160 (1991)
JOURNAL	Mo1. Gen. Genet. 231 (1), 150-160 (1991)
MEDLINE	92092956
PUBMED	1753941
REFERENCE	2 (bases 1 to 623)
AUTHORS	Wu,R.U.
TITLE	Direct Submission
JOURNAL	Submitted (21-MAR-1994) R.U. Wu, Cornell University, Section of Biochemistry Molecular & Cell Biology, 316 Biotechnology Building, Ithaca, NY 14853, USA
FEATURES	Location/Qualifiers
source	1..623
	/organism="Oryza sativa (japonica cultivar-group)"
	/mol_type="genomic DNA"
	/culivar="B-42"
	/sub_species="japonica"
	/db_xref="taxon:39947"
	1..8
TATA_signal	join(42..120,569..623)
gene	/gene="Act1"
	join(42..120,569..>623)
mRNA	/gene="Act1"
	42..120
exon	/gene="Act1"
	/number=1
	/evidence=experimental
	121..568
intron	/gene="Act1"
	/number=1
	569..>623
exon	/gene="Act1"
	/number=2
	/evidence=experimental
	576..>623
CDS	/gene="Act1"
	/codon_start=1
	/product="actin"
	/protein_id="CAA45324.1"
	/db_xref="GI:468506"
	/db_xref="UniProt/TREMBL:O40656"
	/translation="MADADGSGPGQSLM"
	621..623
gene	/gene="Gus"
	621..>623
CDS	/gene="Gus"
	/codon_start=1
	/protein_id="CAA45325.1"
	/db_xref="GI:4379330"
	/translation="M"
ORIGIN	
Query Match	83.6%; Score 379.4; DB 8; Length 623;
Best Local Similarity	93.5%; Pred. No.2,7e-88;
Matches	420; Conservative 0; Mismatches 21; Indels 8; Gaps 2
Oy	6 CACCCGCCCCCTCTCTCTCTCTCTCTCCGTTTTTTTTTCGTCGCTCGATCTTTG 65
Db	128 CCCCAGCCCCCTCTCTCTCTCTCTCCGTTTTTTTTTCGTCGCTCGATCTTTG 187
Oy	66 GCCTTAGTAGTTGGGTGGCGAGCGAGCGGCTTCGTGCGCCAGATCGGTGGCGGAGGAGG 125

Db	188	GCCTTGATGTTGGGGGCGCAGAG-GCGGCTTCCTCCGCCAGATCGGTGCGCGGGAGGGG	246
Qy	126	CGGATCTCCGCGCGCTCGGGGTCTCCGGGCGTGAGTCGGGCCGGATCCCGCGGGGAATGGG	185
Db	247	CGGATCTCCGCGCGCTCGG-----GTCGCGCGTGGCGCGCGGATCTCCGCGGGGAATGGG	299
Qy	186	GCTCTCGAGTGAATCTGATCCGCCGCTGTGTGGGGAGATGATGATGGGCGCTTTAAATTT	245
Db	300	GCTCTCGAGTGAATCTGATCCGCCGCTGTGTGGGGAGATGATGATGGGCGCTTTAAATTT	359
Qy	246	CGCATGCTAAACAAGATCAGAAAGAGGGGAAAAGGCACTATGTTATATTTTAAAT	305
Db	360	CGCATGCTAAACAAGATCAGAAAGAGGGGAAAAGGCACTATGTTATATTTTAAAT	419
Qy	306	ATTTCGTGCTGCTCGTCGACGCTTAAGTGTGCTAAGATCTTTCTTTCTTTTGTGGG	365
Db	420	ATTTCGTGCTGCTCGTCGACGCTTAAGTGTGCTAAGATCTTTCTTTCTTTTGTGGG	479
Qy	366	TGAATTTGAATCCCTCAGCATTTGTCAATCGGTGATTTTCTTTCTTCAATTTGTACAA	425
Db	480	TGAATTTGAATCCCTCAGCATTTGTCAATCGGTGATTTTCTTTCTTCAATTTGTACAA	539
Qy	426	ATGCAGCTCTGTGCGAGACTTTTGTAG	454
Db	540	ATGCAGCTCTGTGCGAGACTTTTGTAG	568

RESULT 11	150114	1392 bp	DNA	linear	PAT 07-OCT-199
LOCUS	Sequence 6 from patent US 5641876.				
DEFINITION	150114				
ACCESSION	150114				
VERSION	150114.1	GI:2472334			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1392)				
TITLE	McELROY, D. and Wu, R.				
JOURNAL	Rice actin gene and promoter				
FEATURES	Patent: US 5641876-A 6 24-UN-1997;				
source	Location/Qualifiers				
	1..1392				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	83.6%;	Score 379.4;	DB 6;	Length 1392;	
Best Local Similarity	93.5%;	Pred. No. 3.1e-88;			
Matches 420;	Conservative 0;	Mismatches 21;	Indels 8;	Gaps 2	
QY	6	CAACCCGCCCCCTCTCCTCTTTCTTTCTCCGTTTTTTTTTTCGATCGGATCTTG	65		
DB	926	CCCCGGTCCCTCTCTCTTTCTTCCTCCGTTTTTTTTTTCGATCGATCTTG	985		
QY	66	GCCTTGGTAGTTGGGTGGGAGACGGCTTCGTCCGCAGATCGGTGCGCGAGGGG	125		
DB	986	GCCTTGGTAGTTGGGGGCGAGAG-GCGGCTTCGTCCGCAGATCGGTGCGCGAGGGG	104		
QY	126	CGGATCTCGCGGCTGGGCTCCCGGGGTGAGTCGGCCCGGATCTCGCGGGAATGGG	185		
DB	1045	CGGATCTCGCGGCTGG-----GTCTCGGCGTGGCGCGGATCTCGCGGGAATGGG	109		
QY	186	GCTCTCGAGTAGATCTGATCCGCGTGTGTGGGGAGATGATGGGGCGTTAAATTT	245		
DB	1098	GCTCTCGAGTAGATCTGATCCGCGTGTGTGGGGAGATGATGGGGCGTTAAATTT	115		
QY	246	CGCAGCTAAACAAGATCAGGAAGAGGGGAAAGGGCACTATGCTTATATTTTATAT	305		
DB	1158	CGCAGCTAAACAAGATCAGGAAGAGGGGAAAGGGCACTATGCTTATATTTTATAT	121		
QY	306	ATTTCGTGCTGCTCGTCAAGCTTAGATGTGCTAGATCTTTCTTTTGTGGG	365		

Db	1218	ATTCTGCGGCTGCTGTCGACGCTTAAGATGTCAGATCTTCTCTTCTTTTGTGGG	1277
Qy	366	TAGAAATTGAATCCCTGACGACATGTTCAATCGGTAATTTTCTTTTCATGATTTGTGCAA	425
Db	1278	TAGAAATTGAATCCCTGACGACATGTTCAATCGGTAATTTTCTTTTCATGATTTGTGCAA	1337
Qy	426	ATGCAGCCTCGGCGGAGCTTTTGTGAG	454
Db	1338	ATGCAGCCTCGTGGGAGCTTTTGTGAG	1366
RESULT 12			
LOCUS	150115	1404 bp	DNA
DEFINITION	Sequence 7 from patent US 5641876.	linear	PAT 07-OCT-1997
ACCESSION	150115		
VERSION	150115.1		GI:2472335
KEYWORDS			
SOURCE	.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1404)		
AUTHORS	McElroy,D. and Wu,R.		
TITLE	Rice actin gene and promoter		
JOURNAL	Patent: US 5641876-A 7 24-JUN-1997;		
FEATURES	Location/Qualifiers		
source	1..1404		
	/organism="unknown"		
ORIGIN	/mol_type="unassigned DNA"		
Query Match	83.6%; Score 379.4; DB 6; Length 1404;		
Beat Local Similarity	93.5%; Pred.No. 3.1e-88;		
Matches	420; Conservative 0; Mismatches 21; Indels 8; Gaps 2;		
Qy	6	CACCCCGCCCTCTCTCTTCTTCTCTCCGTTTCTTTTGTGCTCGGTCGATCTTGG	65
Db	936	CCCCCGCTCCCTCTCTCTTCTCTCCGTTTCTTTTGTGCTCGGTCGATCTTGG	995
Qy	66	GCCTTGATGTTGGGTGGGCGAGAGCGGCTTCGTCGACATCGGCGCGGAGGGG	125
Db	996	GCTTGATGTTGGGTGGGCGAGAG-GCGGCTTCGTCGACATCGGCGCGGAGGGG	1054
Qy	126	CGGAGTCTCGGGGCTGCGCTCCGGGCGTAGTCGCGCCGAGATCCTCGCGGAGATGG	185
Db	1055	CGGAGTCTCGGGGCTG-----GTCGCGGTGCGGCGGATCTCGCGGAGATGG	1107
Qy	186	GCTCGGATGATGATCTGATCCGCCGTTGTGGGGGAGATGAGGGCGTTTAAATTT	245
Db	1108	GCTCGGATGATGATCTGATCCGCCGTTGTGGGGGAGATGAGGGCGTTTAAATTT	1167
Qy	246	CGCCATGCTAAACAAGATCAGAGAAAGGGGAAAGGAGCATAGCTTATAATTTTATAT	305
Db	1168	CGCCATGCTAAACAAGATCAGAGAAAGGGGAAAGGAGCATAGCTTATAATTTTATAT	1227
Qy	306	ATTCTGCTGCTGCTGCTCAGGCTTAGATGTCATGATCTTCTCTTCTTTTGTGGG	365
Db	1228	ATTCTGCTGCTGCTGCTCAGGCTTAGATGTCATGATCTTCTCTTCTTTTGTGGG	1287
Qy	366	TAGAAATTGAATCCCTGACGACATGTTCAATCGGTAATTTTCTTTTCATGATTTGTGCAA	425
Db	1288	TAGAAATTGAATCCCTGACGACATGTTCAATCGGTAATTTTCTTTTCATGATTTGTGCAA	1347
Qy	426	ATGCAGCCTCGGCGGAGCTTTTGTGAG	454
Db	1348	ATGCAGCCTCGTGGGAGCTTTTGTGAG	1376
RESULT 13			
LOCUS	150113	2199 bp	DNA
DEFINITION	Sequence 5 from patent US 5641876.	linear	PAT 07-OCT-1997
ACCESSION	150113		

VERSION	IS0113.1	GI:2472333
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 2199)	
TITLE	McElroy,D. and Wu,R.	
JOURNAL	Rice actin gene and promoter	
FEATURES	Patent: US 5641876-A 5 24-JUN-1997;	
source	Location/Qualifiers 1..2199	
ORIGIN	/organism="unknown"	
	/mol_type="unassigned DNA"	
Query Match	83.6%; Score 379.4; DB 6; Length 2199;	
Best Local Similarity	93.5%; Pred. No. 3,4e-88;	
Matches 420; Conservative	0; Mismatches 21; Indels 8; Gaps 2;	
Dy	6 CACCCGCCCCCTCCTCTTCTTTCTTCGGTTTTTTTTTCGTCCGATCTGCATCTTTTG 65	
Dd	1733 CCCCGCGCTCCCTCCCTCTTCTTCTTCGTTTTTTTTTTCGTCTGATCTTTTG 17922	
Dy	66 GCCTTGAGTTTGCGGCGAGAGAGGGCGCTGTCGCCAGATCGGTGCGCGGAGGGG 125	
Dd	1793 GCCTTGGTAGTTTGGGGGCGAAGA-GCGAGCTTCGTGCCAGATCGGTGCGCGGAGGGG 1851	
Dy	126 CGGAGATCTCGCGCGCTGCGCTCCGGGCGTGAGTCGCGCCGGAATCTCGCGGGAAATGGG 185	
Dd	1852 CGGAGATCTCGCGGCTG-----GTCTCGGCGTGCGGCGGANCTCGGGGGAATGGG 1904	
Dy	186 GCTCTCGAGATGATGATGTGATCCGCGTGTGTGGGGAGATGATGGGCGTTAAAAATT 245	
Dd	1905 GCTCTCGAGATGATCTGATCCGCCGCTGTGTGGGGAGATGATGGGCGCTTTAAAAATT 1964	
Dy	246 CGCATGCTAAACAAGATCAGGAAGAGGGCACTAAGGTTTAATTTTATAT 305	
Dd	1965 CGCATCTTAAACAAGATCAGGAAGAGGGCACTAAGGTTTAATTTTATAT 2024	
Dy	306 ATTCTCTGCTGCTGCTGCTCAGAGCTTAAATGATGATCTTTCTTCTTTTGTGGG 365	
Dd	2025 ATTCTCTGCTGCTGCTGCTCAGAGCTTAAATGATGATCTTTCTTCTTTTGTGGG 2084	
Dy	366 TAGAATTGAATCCCTCAGCAATGTTTCATCGTAGTITTTCTTTCATGATTTGCAA 425	
Dd	2085 TAGAATTGAATCCCTCAGCAATGTTTCATCGTAGTITTTCTTTCATGATTTGCAA 2144	
Dy	426 ATGCAGCCTCTGTGCGGAGCTTTTTTGTAG 454	
Dd	2145 ATGCAGCCTCTGTGCGGAGCTTTTTTGTAG 2173	
RESULT 14		
LOCUS	IS0112	5643 bp DNA linear PAT 07-OCT-1997
DEFINITION	Sequence 4 from patent US 5641876.	
ACCESSION	IS0112	
VERSION	IS0112.1 GI:2472332	
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 5643)	
TITLE	McElroy,D. and Wu,R.	
JOURNAL	Rice actin gene and promoter	
FEATURES	Patent: US 5641876-A 4 24-JUN-1997;	
source	Location/Qualifiers 1..5643	
ORIGIN	/organism="unknown"	
	/mol_type="unassigned DNA"	
Query Match	83.6%; Score 379.4; DB 6; Length 5643;	

Search completed: September 12, 2005, 02:27:05
Job time : 1430.99 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 22:00:56 ; Search time 194.282 Seconds
(without alignments)
13833.284 Million cell updates/sec

Title: US-10-758-799-2

Perfect score: 454
Sequence: 1 GTTACCAACCCGCCCTCTC.....CGTGGAGACTTTTGTAG 454

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	100.0	454	AAZ91038	Aaz91038 Rice acti
2	454	100.0	1565	AAZ91039	Aaz91039 Chimeric
3	402.4	88.6	13680	ADP73931	Adp73931 Plasmid p
4	382.2	84.2	470	ABT07357	Abt07357 Repor
5	382.2	84.2	470	ADP49181	Adp49181 Rice acti
6	379.4	83.6	623	AAZ47117	Aaz47117 Rice acti
7	379.4	83.6	623	ABK66738	Abk66738 Rice acti
8	379.4	83.6	1392	AAZ80053	Aaz80053 Rice acti
9	379.4	83.6	2199	AAZ80052	Aaz80052 Rice acti
10	379.4	83.6	5643	AAZ80055	Aaz80055 Rice acti
11	357.4	78.7	9359	ABK11039	Abk11039 pVDH636 v
12	357.4	78.7	9359	ABK10687	Abk10687 Transform
13	355.8	78.4	491	AAZ51179	Aaz51179 Intron of
14	355.8	78.4	491	ACA05324	Aca05324 Rice acti
15	355.8	78.4	3039	AAZ51644	Aaz51644 Bacillus
16	355.8	78.4	3039	AAZ51645	Aaz51645 Bacillus
17	355.8	78.4	3039	AAZ51793	Aaz51793 Bt.cry3Bb
18	355.8	78.4	3039	AAZ51792	Aaz51792 Bt.cry3Bb
19	355.8	78.4	3039	ABX95189	Abx95189 B. thurin
20	355.8	78.4	3039	ABX95188	Abx95188 B. thurin

21	355.8	78.4	3044	AAZ51656	Aaz51656 Bacillus
22	355.8	78.4	3044	AAD61804	Aad61804 Bt.cry3Bb
23	355.8	78.4	3044	ABX95200	Abx95200 B. thurin
24	355.8	78.4	3450	AAZ51643	Aaz51643 Bacillus
25	355.8	78.4	3450	AAD61791	Aad61791 Bt.cry3Bb
26	355.8	78.4	3450	ABX95187	Abx95187 B. thurin
27	355.8	78.4	3455	AAZ51655	Aaz51655 Bacillus
28	355.8	78.4	3455	AAD61803	Aad61803 Bt.cry3Bb
29	355.8	78.4	3455	ABX95199	Abx95199 B. thurin
30	355.8	78.4	3469	AAZ51646	Aaz51646 Bacillus
31	355.8	78.4	3469	AAD61794	Aad61794 Bt.cry3Bb
32	355.8	78.4	3469	ABX95190	Abx95190 B. thurin
33	355.8	78.4	5170	ADK98488	Adk98488 B. thurin
34	355.8	78.4	5600	ADK98490	Adk98490 B. thurin
35	348	76.7	4032	AAZ73237	Aaz73237 Plasmid p
36	348	76.7	5118	ADP73930	Adp73930 Plasmid p
37	348	76.7	6865	AAZ80287	Aaz80287 Nucleotid
38	348	76.7	7545	ACP58343	Act58343 Nucleotid
39	348	76.7	7943	AAZ80289	Aaz80289 Nucleotid
40	348	76.7	9143	AAZ80286	Aaz80286 Nucleotid
41	348	76.7	10003	AAZ80295	Aaz80295 Nucleotid
42	348	76.7	10003	AAZ80295	Aaz80295 Nucleotid
43	348	76.7	11643	ACP58344	Act58344 Nucleotid
44	340.8	75.1	2181	ADK84543	Adk84543 Rice acti
45	338.4	74.5	2378	AAD01016	Aad01016 Expressio

ALIGNMENTS

RESULT 1	AAZ91038 standard; DNA; 454 BP.
ID	AAZ91038
AC	AAZ91038;
XX	
XX	
XX	06-JUN-2000 (first entry)
DE	Rice actin gene intron 1 sequence.
XX	
XX	Regulatory element; monocotyledonous vegetable plant cell; maize;
KW	histone H3c4; promoter; rice actin gene intron; chimeric; ss;
KM	herbicide resistance.
XX	
XX	Oryza sativa.
OS	
XX	
XX	FR27272787-A1.
PN	
XX	
PD	25-JUN-1999.
XX	
XX	24-DEC-1997; 97FR-00016726.
XX	
XX	24-DEC-1997; 97FR-00016726.
PR	
XX	(RHON) RHONE-POULENC AGROCHIMIE.
XX	
XX	Derose R, Freysinet G;
PI	
XX	WPI; 1999-397352/34.
DR	
XX	5' chimeric regulatory region comprising maize histone H3c4 promoter and
PT	rice actin gene first intron.
XX	
XX	Claim 5; Page 14; 24pp; French.
PS	
XX	The invention relates to a DNA sequence (AAZ91039) comprising a 5'
CC	regulatory element for the expression of a heterologous gene in a
CC	monocotyledonous vegetable plant cell. The DNA comprises: (a) a
CC	functional fragment of the maize histone H3c4 promoter sequence
CC	(AAZ91037); and (b) a functional fragment of the first intron of the rice
CC	actin gene (this sequence). The chimeric regulatory region is useful for
CC	the expression of heterologous genes that confer resistance to certain
CC	herbicides, or that have novel agronomical properties in monocotyledons.

XX	Transgenic plant; immunoglobulin production; recombinant production;
KW	glycosylation; fucose; glycan; virucide; immunotherapy; maize;
KW	gamma-zein promoter; rice; actin promoter;
KW	phosphinothricin acyltransferase; PAT; mouse; leader sequence;
KW	herpes simplex virus; HSV1; HSV2; human; monoclonal antibody HX8; Igh;
KW	heavy chain; light chain; codon optimised; plaamid; PDAB8505; cyclic;
XX	circular; ds.
OS	Zea mays.
OS	Mus sp.
OS	Homo sapiens.
OS	Oryza sativa.
OS	Chimeric.
OS	Synthetic.
OS	Unidentified.
XX	
FT	Key
FT	misc_feature
FT	424..1589
FT	Location/Qualifiers
FT	/*tag= a
FT	/label= SAR
FT	/note= "Scaffold attachment region. Also referred to as
FT	MAR (matrix association region)"
FT	1673..3175
FT	/*tag= b
FT	/note= "Maize gamma-zein promoter"
FT	3178..4671
FT	/*tag= d
FT	/product= "Heavy chain of human anti-HSV1/HSV2 monoclonal
FT	IgA antibody HX8 (with mouse leader sequence)"
FT	3178..3234
FT	/*tag= c
FT	/note= "Mouse leader sequence"
FT	3235..4668
FT	/*tag= e
FT	/product= "Mature HX8 heavy chain"
FT	4678..5045
FT	/*tag= f
FT	/note= "Maize per5 3'UTR"
FT	5157..6659
FT	/*tag= g
FT	/note= "Maize gamma-zein promoter"
FT	6662..7363
FT	/*tag= i
FT	/product= "Heavy chain of human anti-HSV1/HSV2 monoclonal
FT	IgA antibody HX8 (with mouse leader sequence)"
FT	6662..6718
FT	/*tag= h
FT	/note= "Mouse leader sequence"
FT	6719..7360
FT	/*tag= j
FT	/product= "Mature HX8 heavy chain"
FT	7370..7737
FT	/*tag= k
FT	/note= "Maize per5 3'UTR"
FT	7889..9258
FT	/*tag= l
FT	/note= "Rice actin promoter/intron"
FT	9261..9815
FT	/*tag= m
FT	/product= "Phosphinothricin acyltransferase (PAT)"
FT	/note= "The PAT coding region is given in the
FT	specification as positions 9260-9820"
FT	9831..10162
FT	/*tag= n
FT	/note= "Maize lipase 3'UTR"
FT	10229..11394
FT	/*tag= o
FT	/label= SAR
FT	/note= "Scaffold attachment region. Also referred to as
FT	MAR (matrix association region)"
XX	
XX	MO2004050838-A2.

PD	17-JUN-2004.
XX	
PF	28-NOV-2003; 2003WO-USO37905.
PR	
XX	27-NOV-2002; 2002US-0429385P.
PA	(DOMC) DOM CHEM CO.
PA	(DOMC) DOM AGROSCIENCES LLC.
PA	(EPIC-) EPICYTE PHARM INC.
PI	Birgys K, Giancy T, Hein MB, Hiatt AC, Karnoup AL, Anderson WHK;
PI	Paredy D, Petelin J, Rubin-Wilson B, Taylor D, Roberts JL,
XX	
DR	WP1: 2004-461111/43.
DR	P-PSDB; ADP73848, ADP73856.
PT	
PT	Novel plant-produced immunoglobulin having glycopeptide or glycan profile
PT	with reduced fucoylation, useful for treating herpes simplex virus
PT	infection.
XX	
PS	Claim 69; SEQ ID NO 85; 212pp; English.
CC	
CC	The invention relates to the production of immunoglobulins in plants,
CC	wherein at least a portion of the glycans attached to the immunoglobulins
CC	lack fucose. The immunoglobulins produced can be of any class (i.e., IgG,
CC	IgA, IgM, IgE or IgD) and is especially an anti-herpes simplex virus
CC	(HSV) antibody or an anti-alphaHerpes3, alphaHerpes dual integrin
CC	antibody. The invention also relates to constructs, plasmids and vectors
CC	for producing the immunoglobulins; transformed plant cells, calli, plant
CC	tissues and whole plants for producing the immunoglobulins; methods for
CC	producing the immunoglobulins, the immunoglobulins thus produced; and the
CC	use of such immunoglobulins. The immunoglobulins of the invention may be
CC	used to treat HSV infection or tumour angiogenesis. The invention
CC	provides the advantages of antibody production in plants, such as large
CC	scale production, reduced costs, and elimination of pathogenic
CC	contaminants such as viruses and prions, with a simplified (i.e., non-
CC	plant-specific) glycosylation profile which reduces the risk that the
CC	immunoglobulin may not be functional in animals. The present sequence
CC	represents the plasmid pDAH8505, which contains codon optimised DNA
CC	sequences encoding the heavy and light chains of the human anti-HSV1/HSV2
CC	monoclonal IgA antibody HX8 each of which are fused to mouse leader
CC	sequences. Both heavy and light chain fusion genes are under the control
CC	of maize endosperm-specific gamma-zain promoters. The plasmid also
CC	contains a phosphinothricin acyltransferase (PAT) gene under the control
CC	of a rice actin promoter.
XX	
SQ	Sequence 13680 BP; 3886 A; 3069 C; 2934 G; 3788 T; 0 U; 3 Other;
	Query Match 88.6%; Score 402.4; DB 12; Length 13680;
	Best Local Similarity 98.0%; Pred. No. 5.3e-104;
	Matches 451; Conservative 0; Mismatches 1; Indels 8; Gaps 4;
OY	1 GTAACCAACCGGCCCTCTCTCTTTTCTTTTCTTCGGTTTTTTTGCTGCCTCAT 60
DB	8796 GTAACCAACCGGCCCTCTCTCTTTTCTTTTCTTCGGTTTTTTTGCTGCCTCAT 8855
OY	61 CTTGGGCTTGATGTGGGTGGGAGAGCGGCTCGTCCCAATGGTGGCGGG 120
DB	8856 CTTTGGCTTGATGTGGGTGGGAGAGCGGCTCGTCCCAATGGTGGCGGG 8915
OY	121 AGGAGCGGGAATCTGCGCGCTGCGCTTCGCGGCGTAGTGGGCCCGATCCTCGCGGGGA 180
DB	8916 AGGAGCGGGAATCTGCGCGCTGCGCTTCGCGGCGTAGTGGGCCCGATCCTCGCGGGGA 8975
OY	181 ATGGGGCTCTCGATGTAGATCT--GATCCGCGCTTGTGGGGAGAATATGGGGCTTT 238
DB	8976 ATGGGGCTCTCGATGTAGATCTCGCAATCCGCCCTTGTGGGGAGAATATGGGGGATT 9035
OY	239 AAAATTT-CGCAATGATAACAAGATCAGGAAAGGGGAAAGGGCACTATGGTTATAT 297
DB	9036 AAAATTTCCGCAATGATAACAAGATCAGGAAAGGGGAAAGGGCACTATGGTTATAT 9095
OY	298 TTATATATTTCTGCTGCTGCTGTCGAGGCTTAAGATGTGCTAGA--TCTTTTCTT 354

Qy	Dy	Qy	Dy
355	9096	415	9214
CTTTTGGGGAGAAATTGAAATCCCTAGACATGTTATCGGTATTTTCTTTTCATG	TTTATATATATTTTCGCTGCT--TCGTACGGCTTAAATGTCATGATCTTCTTTCTTTCTT	ATTGTGTGACAAATGACGCTCGTGTGGAGCTTTTGTGAG	ATTGTGTGACAAATGACGCTCGTGTGGAGCTTTTGTGAG
9154		9214	
CTTTTGTGGGGAGAAATTGAAATCCCTAGACATGTTATCGGTATTTTCTTTTCATG			
9154		9214	
CTTTTGTGGGGAGAAATTGAAATCCCTAGACATGTTATCGGTATTTTCTTTTCATG			

RESULT 4
ABT07357
ID ABT07357 standard; DNA; 470 BP.

DT 07-NOV-2002 (first entry)

Reporter construct rice actin intron SEQ ID NO: 109.

KW Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor; ds.

Oryza sativa.

PN WO200261102-A2.

PD 08-AUG-2002.

PF 24-OCT-2001; 2001WO-US051417.

PR 24-OCT-2000; 2000US-0242969P.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

DR WPI; 2002-619259/66.

PT New receptor cassette encoding a chimeric receptor polypeptide, useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility.

PS Example 10; Page 263; 319pp; English.

The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecdysone receptor (EcR) of an insect, a ligand binding domain of an insect EcR, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The present sequence is a polynucleotide described in the exemplification of the invention

Sequence 470 BP; 75 A; 103 C; 141 G; 151 T; 0 U; 0 Other;

Query Match 84.2%; Score 382.2; DB 6; Length 470;

Matches 433; Conservative 0; Mismatches 13; Indels 13; Gaps 3;

QY 1 GTACCACCCGCCCTCTCTTCTTCTTCTCCGTTTTTTTTT-CGTCTCGGTCTCGA 59

Db 4 GTACCAACCCGCCCTCTCTCTTCTTCTTCTCCGTTTCTTCTCCGTCCTCGGTCGA 63

60 TCTTTGGCCTTGGTAGTTTGGGTGGCGAGA---GCGGCTTCGTCGCCCAGATCGGTGC 115

Db 64 TCTTTGGCCTTGGTAGTTGGGTGGCGAGAGCGGCTTCGTGCGCGCCAGATCGGTGC 123

QY	116	GCGGAGAGGGCGGGATCTTCGCGGCTCGGCTCTCCGGCGTGAATCGGGACCGGATCCCGC	175
Db	124	GCGGGAGGGGCGGGATCTTCGCGGCTG-----GGGCTTCGCGCGCGTGGATCTTCGC	175
QY	176	GGGGAATGGGGGCTCCGAGTGTGAATCTGAATCCGCGCGTGTGGGGAGATGATGGGGCG	235
Db	176	GGGGAATGGGGGCTTCGAGTGTGAATCTGAATCCGCGTGTGGGGAGATGATGGGGCG	235
QY	236	TTTAAATTTCCGCAATGCTAAACAAGATCAGAGAGGGGAAAAGGCACTATGTTTAT	295
Db	236	TTTAAATTTCCGCAATGCTAAACAAGATCAGAGAGGGGAAAAGGCACTATGTTTAT	295
QY	296	ATTTTATATATTTCTGCTGCTGCTCGTCAAGCTTAAATGTCTGATCTTTCTTCTTC	355
Db	296	ATTTTATATATTTCTGCTGCTGCTCGTCAAGCTTAAATGTCTGATCTTTCTTCTTC	355
QY	356	TTTTTGTGGGTGAATTTGAATCCCTCAAGCATTTTCATCGGTAGTTTTCTTTCAATGA	415
Db	356	TTTTTGTGGGTGAATTTGAATCCCTCAAGCATTTTCATCGGTAGTTTTCTTTCAATGA	415
QY	416	TTTGTGAACAATGCAAGCTTCGTGGGAGCTTTTGTAG	454
Db	416	TTTGTGAACAATGCAAGCTTCGTGGGAGCTTTTGTAG	454

RESULT 5	
ADDF49181	
ID	ADDF49181 standard; DNA; 470 BP.

AC ADF49181;

DT 12-FEB-2004 (first entry)

DE Rice actin intron.

KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;

KW activation domain; transgenic seed; transgenic plant; plant line;

XX

OS *Oryza* sp.

PN US2003154509-A1.

PD 14-AUG-2003.

PF 24-OCT-2001; 2001US-00087167

PR 24-OCT-2001; 2001US-00087167.

PA (PASC/) PASCAL E J.

PA (BROW/) BROWN J A.

PA (JOHN/) JOHNSON B D.

PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

DR WPI; 2003-897756/82.

PT New receptor cassette encoding a chimeric receptor polypeptide, useful

PT presence of appropriate chemical ligands.

PS Example 10; SEQ ID NO 109; 186bp; English..

CC The invention describes a receptor cassette encoding a chimeric receptor
CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
CC (D) domain of an ecdysone receptor (EcR), a ligand binding
CC (E) domain that is heterologous with respect to the D domain, and an
CC activation domain. The receptor cassette and method are useful in
CC regulating the expression of target polypeptides in plants in the
CC presence of appropriate chemical ligands. The transgenic seeds and plants

OY	306	ATTTCGCGCGCTGCTGCTGAGCTTATGAGTGTGATATCTTCTTCTTTGAGG	365
Db	420	ATTTCGCTGCTGCTGCTGCTGAGCTTATGAGTGTGATATCTTCTTCTTTGAGG	479
OY	366	TAGAAATTTGAATCCCTCAGCAATGTTTCATCGTAGTCTTTTCTTTTCATGATTTGTGACA	425
Db	480	TAGAAATTTGAATCCCTCAGCAATGTTTCATCGTAGTCTTTTCTTTTCATGATTTGTGACA	539
OY	426	ATGCAGCCTCGTGGGAGCTTTTGTAG	454
Db	540	ATGCAGCCTCGTGGGAGCTTTTGTAG	568
RESULT 7			
ID	ABK86738	standard; DNA; 623 BP.	
AC	ABK86738;		
XX			
DT	24-SEP-2002	(first entry)	
XX			
DE	Rice Act1 gene.		
XX			
KW	Rice; gene; db; transgenic; plant; lignocellulose; cellulase; ligninase;		
KW	fermentable sugar; ethanol; fermentation; silage; feed; fuel;		
KW	industrial chemical; biodegradation; chloroaromatic;		
KW	environmental pollutant; Act1.		
XX			
OS	Oryza sativa.		
XX			
PN	WO200234926-A2.		
XX			
PD	02-MAY-2002.		
XX			
PF	18-OCT-2001; 2001WO-US032538.		
XX			
PR	20-OCT-2000; 2000US-0242408P.		
XX			
PA	(UNMS) UNIV MICHIGAN STATE.		
XX			
PI	Sticklen MB, Dale BE, Magpool S;		
DR	WPI; 2002-489947/52.		
XX			
PT	Producing transgenic plants which after harvest degrade lignin and		
PT	cellulose to fermentable sugars, by mating transgenic plant comprising		
PT	DNA encoding cellulase with transgenic plant comprising DNA encoding		
PT	ligninase.		
XX			
PS	Example 1; Page 124; 126pp; English.		
XX			
CC	The invention discloses the production of a transgenic plant which		
CC	degrades lignocellulose when the plant is ground. It comprises the		
CC	production of the transgenic plant including cellulase and ligninase by		
CC	mating a transgenic plant, containing a DNA encoding a cellulase, and a		
CC	transgenic plant, containing a DNA encoding a ligninase, where both genes		
CC	are operably linked to a nucleotide sequence encoding a signal peptide		
CC	which targets the fusion protein to an organelle of the plant,		
CC	particularly chloroplasts. The method is useful for producing a		
CC	transgenic plant (e.g. maize) which degrades lignocellulose when the		
CC	plant is ground to produce a plant material. This material is useful for		
CC	converting lignocellulose, in a plant material, to fermentable sugars		
CC	which are then fermented to ethanol. The transgenic plants also provide a		
CC	plentiful and inexpensive source of fungal or bacterial cellulases and		
CC	ligninases which can be used in the production of ethanol. They can also		
CC	be used for pre-treating silage to increase the energy value of		
CC	lignocellulosic feeds for cows and other ruminant animals, pre-treating		
CC	lignocellulosic biomass for fermentative conversion to fuels and		
CC	industrial chemicals, and biodegradation of chloroaromatic environmental		
CC	pollutants. The sequence presented is the rice Act1 gene and promoter		
XX			
Sequence	623 BP; 98 A; 184 C; 164 G; 177 T; 0 U; 0 Other;		

[illegible]

RESULT 8	
AA780053	
ID	AA780053 standard; cDNA; 1392 BP.
XX	
AC	AA780053;
XX	
DT	25-MAR-2003 (revised)
DT	04-NOV-1997 (first entry)
XX	
DE	Rice actin 1 gene promoter fragment.
XX	
KW	Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth
KW	cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.
XX	
OS	Oryza sativa.
XX	
PN	US5641876-A.
XX	
PD	24-JUN-1997.
XX	
PF	27-OCT-1993; 93US-00144602.
XX	
PR	05-JAN-1990; 90US-00461490.
PR	18-SEP-1991; 91US-00762680.
XX	
PA	(CORR) CORNELL RES FOUND INC.
XX	
PI	Wu R, Mcelroy D;
XX	
DR	WPI, 1997-340996/31.
XX	
PT	Nucleic acid containing the promoter of the rice actin-1 gene - used to
PT	direct efficient expression of foreign genes in rice.
XX	
PS	Claim 4; Col 35-38; 29pp; English.
XX	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 23:36:11 ; Search time 1190.88 Seconds
(without alignments)
14511.284 Million cell updates/sec

Title: US-10-758-799-2

Perfect score: 454
Sequence: 1 GTTACCAACCCGCCCTCTC.....CGTGGAGCTTTTGTAG 454

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 segs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116.4	25.6	542	5	BQ609717 BRY_5803
2	53.2	11.7	922	9	CNS0073W AL066784 Drosophi1
3	53.2	11.7	1083	9	AG429940 Mus muscu
4	52.8	11.6	1013	9	CNS016KT AL106871 Drosophi1
5	51.8	11.4	895	9	CNS0071A AL066286 Drosophi1
6	51.6	11.4	884	9	CNS006U0 AL065923 Drosophi1
7	51.2	11.3	919	9	CNS006S5 AL065856 Drosophi1
8	50	11.0	686	8	BZ031798 oel99D01.1
9	49.4	10.9	789	9	B1886452 ZF637-1-0
10	48.6	10.7	909	9	CNS00JTL AL076720 Drosophi1
11	47.6	10.5	1036	9	CNS010BS AL098770 Drosophi1
12	47.6	10.5	1656	9	CL496209 SATL_620
13	46.2	10.2	822	9	CNS009CW AL053618 Drosophi1
14	46	10.1	1101	9	AL108460 Drosophi1
15	45.6	10.0	602	7	CV131848 L3P0904
16	45.4	10.0	718	9	AG605189 Mus muscu
17	45.2	10.0	951	8	AZ672893 ENTJ74TF
18	44.5	9.9	1101	9	CNS00397 AL063912 Drosophi1
19	44.6	9.8	335	4	B1849271 476584 MA
20	44.6	9.8	889	9	CL484887 SATL_404
21	44.2	9.7	1244	9	AG390554 Mus muscu
22	44	9.7	836	9	AG359094 Mus muscu
23	44	9.7	1100	9	CNS00G3S AL071398 Drosophi1
24	44	9.7	1101	9	CNS00BNG AL057398 Drosophi1

C	25	43.6	9.6	827	6	CB945739	CB945739	AGENCOURT
C	26	43.6	9.6	1083	4	BG786263	BG786263	SRALIMC006
C	27	43.6	9.6	1101	9	CNS014Y2	AL104756	Drosophi1
C	28	43	9.5	658	9	CNS06V94	AL416846	T7 end of
C	29	43	9.5	727	9	AG122958	AG122958	Pan trogl
C	30	43	9.5	1151	9	CNS024YU	AL161216	Tetradon
C	31	42.8	9.4	995	5	B0876303	B0876303	AGENCOURT
C	32	42.8	9.4	1003	1	AL569374	AL569374	AL569374
C	33	42.8	9.4	1101	9	CNS00H28	AL074533	Drosophi1
C	34	42.8	9.4	1130	9	AG176166	AG176166	Pan trogl
C	35	42.6	9.4	583	5	BP316620	BP316620	BP316620
C	36	42.4	9.3	181	2	AM449874	AM449874	UI-H-B13-
C	37	42.4	9.3	384	7	CF098527	CF098527	OHNT011.Y
C	38	42.4	9.3	634	8	AZ574188	AZ574188	325PvG12
C	39	42.4	9.3	715	9	CL598191	CL598191	OB_Ba006
C	40	42.4	9.3	747	9	AG514518	AG514518	Mus muscu
C	41	42.4	9.3	842	9	CNS023AE	AL179244	Tetradon
C	42	42.4	9.3	987	9	CNS004EE	AL051333	Drosophi1
C	43	42.4	9.3	1101	9	CNS0170G	AL108298	Drosophi1
C	44	42.4	9.3	1209	9	CL486043	CL486043	SATL_426
C	45	42.2	9.3	864	9	AG141680	AG141680	Pan trogl

ALIGNMENTS

RESULT 1
BQ609717
LOCUS
DEFINITION BQ609717 542 bp mRNA linear EST 25-JUN-2002
BRY 5803 wheat EST endosperm library Triticum aestivum cDNA 5',
mRNA sequence.
ACCESSION BQ609717 GI:21559056
VERSION BQ609717.1
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 542)
REFERENCE Clarke,B., Lambrecht,M. and Rhee,S.Y.
Arabidopsis genomic information for interpreting wheat EST
sequences
JOURNAL Func. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 22478026
PUBMED 12590341

COMMENT

Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.
Location/Qualifiers

FEATURES

source
1..542
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wyuna"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/clone_lib="wheat EST endosperm library"

ORIGIN

Query Match 25.6% Score 116.4; DB 5; Length 542;
Best Local Similarity 94.1%; Pred. No. 1.2e-19;
Matches 143; Conservative 0; Mismatches 6; Indels 3; Gaps 2;
QY 195 TGTGATCTGATCCCGCTGTTGGGAGATGATGCGGCGTTTAAATTT-CGCCATCC 253
DB 96 TGTGATCTGATCCCGCTGTTGGGAGATGATGCGGCGTTTAAATTTCCGCATCC 155

QY 254 TAAACAAGATCAGAGAGAGGAGGACATGTTATATTTATATATTTCTGC 313
|||||
Db 156 TAAACAAGATCAGAGAGGAGGAGGACATGTTATATTTATATTTCTGC 215
QY 314 TCGTCTCGTACGCTTAAGTGTAGATCT 345
|||||
Db 216 TCGTCTCGTACGCTTAAGTGTAGATCT 245
RESULT 2
CNS0073W 922 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR14D09 of RPCI-98 library from Drosophila melanogaster (fruit
fly); genomic survey sequence.
ACCESSION AL066784 GI:4945247
VERSION AL066784.1
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 922)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammose in Peter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp; the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source
1..922
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="BACR14D09"
/clone_1ib="RPCI-98"
/note="end : TET3"
ORIGIN
Query Match 11.7%; Score 53.2; DB 9; Length 922;
Best Local Similarity 20.3%; Pred. No. 0.0045;
Matches 74; Conservative 128; Mismatches 163; Indels 0; Gaps 0;
QY 36 TTTTCTTTTTCGTCGCTCGATCTTTGACCTTGTAGATTGGCGGAGAGCGC 95
|||||
Db 542 KTTTCTTTTTCGTCGCTCGATCTTTGACCTTGTAGATTGGCGGAGAGCGC 601
QY 96 TTGCTGCGCCAGATCGGTGCGGAGGCGGAGATCCCGCTCGCGCGCCT 155
|||||
Db 602 GTTCTTTTTCGTCGCTCGATCTTTGACCTTGTAGATTGGCGGAGAGCGC 661
QY 156 GAGTCGCGCCGAGATCCGCGGAGGAGATGGGCTCTCGAGATGATCGCGCGCTG 215
|||||
Db 662 TKTTKKKKKTKGKKKKTKGKKGKTGKTGTTGGGAGGAKTKKTTTKTTTK 721
QY 216 TTGGGAGAGATGAGGCGCTTTAAATTTCCGATGCTAAACAAGATCAGAGAGG 275
|||||
Db 722 KKKKTTTKTKTKTKTKTKTKTKTKGKTGKGGKGGKTKGTGTTKKKGKGGK 781

QY 276 AAAAGGACATGTTATATTTATATATTTCTGCTGCTGCTCAGGCTAGATG 335
|||||
Db 782 KKKKKKKKKKKTKGKTGKTGKTGKTGKTGKTGKTGKTGKTGKTGKTGKTG 841
QY 336 TCGTAGATCTTTCTTCTTCTTTTGGGAGTAGAATTCCTCAGCATGTTATC 395
|||||
Db 842 KKKKKGTTGKTKTKTKTKTKTKTKTKTKGKKKKKKGKKKKKKGKKGKKGKK 901
QY 396 CGTAG 400
|-:-|
Db 902 GKKKG 906
RESULT 3
AG429940 1083 bp DNA linear GSS 03-JUN-2004
LOCUS Mus musculus molossinus DNA, clone:MSMg01-304M02.TU, genomic survey
DEFINITION sequence.
ACCESSION AG429940 GI:48073003
VERSION AG429940.1
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1083)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
1-7-22 Suenho-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:<http://hgp.gsc.riken.go.jp/>,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@tc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyada, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@tc.riken.jp
PRIMERS
Sequencing : TU
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : BclRI.
FEATURES
source
1..1083
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-304M02.TU"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_1ib="MSMg01 Mouse Male BAC library"
ORIGIN
Query Match 11.7%; Score 53.2; DB 9; Length 1083;
Best Local Similarity 45.4%; Pred. No. 0.0046;
Matches 187; Conservative 0; Mismatches 225; Indels 0; Gaps 0;
QY 9 CCGGCCCCCTCTCTCTTCTCTCTCGTTTCTGTCGCTCGATCTTTCGCGC 68
|||||
Db 234 CGGCTGTCGTTTCTTCTTCTGCGGCTTTTCTGTTTCTGTTTCTGTTTCTG 293
QY 69 TTGTAATTGGGTGGCGAGAGCGGCTTCTGTCGCCAGATCGTGGCGGAGGCGG 128
|||||

D_b 294 TGGTTTTTTTGTGAGGGGGCGCGCGGGGGGGGGGGGGGGGGCCGCCCGGAGGGCG 353

Q_y 129 GATCTCGGCGCTGCGCTTCGCGGGGCTGAATGCTCGCCGGATCTCTCGCGGGAAATGGGGCT 188

D_b 354 GCGCGGGGGGGGGGGGGCGCGCGGGGGGGGGGGGGGGCGGGGGCGGGGGGGGTTTGCGGGG 413

Q_y 189 CTCGATCTAGATCTGATCCGCCTGTGTGGGGGAGATAGTGGGCGCTTTAAAAATTTCG 248

D_b 414 GCGGGGGGGCGGGGGGGGGCGCGGGGGGGGGGGCGCGGTGCGGGGGGGGGGGCGGGGG 473

Q_y 249 CATCTTAACAAGAATCAGGAAGAGGGGAAAAGGCGACTATGGTTAATTTTATAATT 308

D_b 474 GGCGGTGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGTTTTTTTTTTTTTTTTTTTT 533

Q_y 309 TCTGCTGCTGCTGTCAGGCTTAGATGCTAGATCTTTCTTTCTTTTGTGGTAG 368

D_b 534 TTGTGTTTTTTTGTGTTTTTTTTTTGTTTTTTTTTTTTTTTTTTGTGTTTTTTT 593

Q_y 369 AATTGAATCCCTCAGCATGTGTACATCGTAGTTTTCTTTCAATGATTTGT 420

D_b 594 TTCGTGTGTTTTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 645

RESULT 4					
CNS016KT/c					
LOCUS		1013 bp	DNA	linear	GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence SP6 end of BAC				
	BACN1616 of DrosBac library from Drosophila melanogaster (fruit fly), genomic survey sequence.				

ACCESSION	AL106871
VERSION	AL106871.1
KEYWORDS	GI:5624218
SOURCE	GSS.
ORGANISM	Drosophila melanogaster (fruit fly)
REFERENCE	Drosophila melanogaster
AUTHORS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peirysgota;
TITLE	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
JOURNAL	Ephydroidea; Drosophilidae; Drosophila.
	1 (bases 1 to 1013)
	Genoscope.
	Direct Submission
	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage

COMMENT

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

```

FEATURES
    source
        location/Qualifiers
            1..1013
                /organism="Drosophila melanogaster"
                /mol_type="Genomic DNA"
                /db_xref="taxon:7227"
                /clone="BACNIC16"
                /clone_1lb="DrosBAC"
                /plasmid="pBelobAC11"
                /note="end : Sp6"

```

Query Match	11.6%	Score 52.8	DB 9	Length 1013
Best Local Similarity	24.1%	Pred. No. 0.0058		
Matches 105; Conservative 105; Mismatches 222;				
			Indels 3	Gaps 1;

[illegible]

Oy	138	GCTGGCGCTCTCCGAGGCGCTAAGTCGCACCGATCCTCGCGGGGAATGGAGGCTCTCGAATGT	197
Db	338	NCCCNNAANAACKKKXDDPAACKCCNANNCAAGTKTAKCCGNNKBKKSKKKKNKGSGGG	279
Oy	198	AGATCTGATCCGCCGTGTGTGGGGGAGATGATGGGGCGTTTAAATAATTGCCATGCTAAA	257
Db	278	NKGGKKKSXGGGGSGRSKKGNKNGGSSKKAKGSKSGKGGKKKKKKRNCAAGGKRGGG	219
Oy	258	CAAGATCAGAGAAGGAAAAAGGCACTATGGTTTAATTATTATTAATTTCGTGCT	317
Db	218	-- -- KKKGGGGLTANMKKKKAACA CTNNCTNNKTCTCTTTBT TTTTATCBTTTTT	162
Oy	318	GCTCGTAGCGCTTAGATGTCGTAGACTTTCTTTCTTTCTTTTGSGTAGAATTGAAT	377
Db	161	TTKTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNCTNNSTNCNTNATNTNTNTT	102
Oy	378	CCCACACATTTGTCATCGTAGTTTCTTTTCATGATTTGGACAAATGACACCTCGT	437
Db	101	CTBTTCABTTTTYNTNINCNBTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNTNTGAGT	42
Oy	438	GCGGAGCCTTTTNGT	452
Db	41	TTNACTTTTTTNGT	27

RESULT 5					
CNS0071A		895 bp	DNA	linear	GSS 03-JUN-1999
LOCUS					
DEFINITION	Drosophila melanogaster genome survey sequence TBT3 end of BAC # 17				

ACCESSION	AL066286	
VERSION	AL066286.1	GI:4945153
KEYWORDS	GSS.	
SOURCE	Drosophila melanogaster	(fruit fly)
ORGANISM	Drosophila melanogaster	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 895)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqret@genoscope.cns.fr
- Web : www.genoscope.cns.fr/)
Determination of this BAC-end sequence was carried out as part of a

COMMENT

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuhiro Oosagawa and Aaron Mammeter in Pierer de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RP11-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	Location/Qualifiers
source	1..895

ORIGIN	
Query Match	11.4%; Score 51.8; DB 9; Length 895;
Best Local Similarity	20.5%; Pred. No. 0.011;

[illegible]

RESULT 6	
CNS006UO	884 bp DNA linear GSS 03-JUN-1999
LOCUS	
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14W21 of RPci-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL065923
VERSION	AL065923.1 GI:4944891
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 884) Genoscope.
REFERENCE	Direct Submission
AUTHORS	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr
TITLE	- Web : www.genoscope.cns.fr)
JOURNAL	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutyo Osoegawa and Aatron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila.bac.htm .
COMMENT	

```
FEATURES
    source
        location/Qualifiers
            1..884
                /organism="Drosophila melanogaster"
                /mol_type="genomic DNA"
                /db_xref="taxon:7227"
                /clone="BACR14N21"
                /clone_1fb="RPC1-98"
```

```

ORIGIN                               /note="end : T7"

Query Match          11.4%  Score 51.6;  DB 9;  Length 884;
Best Local Similarity 18.3%  Pred. No. 0.012;
Matches 67; Conservative 139; Mismatches 161; Indels 0; Gaps 0

```

[illegible]

RESULT 7	
CNS006S5	
LOCUS	CNS006S5 919 bp DNA linear GSS 03-JUN-1994
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14J09 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL065856
VERSION	AL065856.1 GI:4944824
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE AUTHORS TITLE JOURNAL	COMMENT
1 (bases 1 to 919) Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr - Web : www.genoscope.cns.fr)	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mamosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila.bac.htm .

FEATURES	Locatio
source	1. .919

OY		5	CCACC CCCCCTC TCCTTCTTTCTTCGTTTTTTTGCGTCTGCATCTTT	64
Dd		992	BSCGSCSSSSSGCGCTTTTCTTTTGTCKCSBSSTTTTCGMGCKSSTGNGTCCGCSCTTY	923
OY		65	GCGCTTGAGATTGGATGGAGACGCGCTTCGTCCGCCAAGATCGGTGGCGGAGG	124
Dd		922	YGCTYTSGCYTTTBSCCSCSSCSCSTXTKGCCSSCSSASCBSTSTTSCGCSHSS	863
OY		125	GCGGAGTTCGCGCTGCGCTTCGCGGCGGTGATCGGCCCGCATCTTCGCGGGAATGC	184
Dd		862	GCKGSCSSGCGCGSSGSGGCTCGSBGCKCGGCSBSSBTGCSGSBGCSBSTRTCTTWS	803
OY		185	GGCTTCGGATGTAGATCGATCCGCGCTTGCTGGGGAGATGAT	229
Dd		802	TGSSGSSSTTKCGSCKCSGCGSGSGTGBSGSGCGCGGBT	758
RESULT_12				
CL496209/C				
LOCUS	CL496209	1656 bp	DNA	linear GSS 01-APR-2004
DEFINITION	SAIL_620_H08.v1 SAIL Collection Arabidopsis thaliana genomic clone			
ACCESSION	SAIL_620_H08.v1,			genomic survey sequence.
VERSION	CL496209_			
KEYWORDS	CL496209.1 GI:45988295			
SOURCE	GSS.			
ORGANISM	Arabidopsis thaliana (thale cress)			
REFERENCE	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie. 1 (bases 1 to 1656) Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D., Dietrich,B., Ho,P., Bacmaden,J., Ko,C., Clarke,J.D., Cotton,D., Bullis,D., Shelli,J., Miguelt,T., Hutchison,D., Kimmerly,B., Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A. A high-throughput Arabidopsis reverse genetics system Plant Cell 14 (12), 2985-2994 (2002)			
AUTHORS				
JOURNAL				
MEDLINE				
PUBMED	12468722 22356987			
COMMENT	Contact: Sessions A Applied Trait Genetics Syngenta Biotechnology Inc. 3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA Email: allen.sessions@syngenta.com ABRC Stock Number CS826580; T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and not single contiguous sequences. Class: TDNA tagged.			
FEATURES				
Source	Location/Qualifiers			
	1..1656			
	/organism="Arabidopsis thaliana"			
	/mol_type="Genomic DNA"			
	/ecotype="Columbia"			
	/db_xref="taxon:3702"			
	/clone="SAIL_620_H08.v1"			
	/clone_jib="SAIL_Collection"			
	/note="T-DNA left border sequences were isolated using a modified TAIL-PCR strategy"			
ORIGIN				
Query Match	10.5%:	Score 47.6;	DB 9;	Length 1656;
Best local similarity	51.2%;	Pred. No. 0.14;		
Matches	104;	Conservative 0;	Mismatches 99;	Indels 0;
			Gaps 0;	
OY		5	CCACCCGCGCCCTCTCTCTTCTTTCTTCGTTTTTTTGCTGCGTCTCAACTTT	64
Dd		451	CCCCCCCCCTTCACACCCCGGCGCCCGTTCCTCTTTGTTCGGTCTTTTCTTT	392
OY		65	GCGCTTGAGATTGGGATGGAGACGCGCTTCGTCCGCCAAGATCGGTGGCGGAGG	124
Dd		391	CCTTCTTTTGTGTGGGTGGGNTTGTGTGTGCGGCGCGTGTGTGNCGCGGCGGGGGG	332

QY	125	GCGGAGATCTGGCGGCTGACCCGTCCTCGGAGCAGTCTCGCGGGAATNG	184
Db	331	GGGTGCTTGCGGCCGCAGCGAGGAGNCCGCTGCGCGGCGCGGCGGCGCTGT	272
QY	185	GGCTCTCGAGTAGTAATCTGATC	207
Db	271	CGTTGTGCTTGTTGTTNGTTTTC	249
RESULT 13			
CNS009CW			
LOCUS			
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC # BACR1H24 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
ACCESSION CNS009CW			
VERSION AT053618			
KEYWORDS AL053618.1 GI:4934864			
SOURCE GSS.			
ORGANISM Drosophila melanogaster (fruit fly)			
Drosophila melanogaster			
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
REFERENCE 1 (bases 1 to 822)			
AUTHORS Genoscope.			
TITLE Direct Submission			
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FR/NMCR (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)			
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by Buffalo EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.			
FEATURES			
SOURCE location/Qualifiers			
1..822			
/organism="Drosophila melanogaster"			
/mol_type="genomic DNA"			
/db_xref="taxon:7227"			
/clone="BACR19H24"			
/clone_lib="RPCI-98"			
/note="end : T7"			
ORIGIN			
Query Match 10.2%; Score 46.2; DB 9; Length 822;			
Best Local Similarity 38.7%; Pred. No. 0.31;			
Matches 138; Conservative 32; Mismatches 187; Indels 0; Gaps 0;			
QY	64	TGCGCTTGATGTTGGGTGGCGAGAGCGGCTTCGTGCCCCAGATCGTGC CGGAGG	123
Db	312	TKGGGKGBGGGTGGGGGGGTGGGTGGGGGGGGGGGTGTGKGKGTGKKGTGTG	371
QY	124	GGCGGATCTCGCGCTGCGCTCTCCGGGCGTGA GTGGCCCGATCTCGCGGGAGT	183
Db	372	GG	431
QY	184	GGGCTCTCGAGTAGAATTGATCCGCCGTTGTTGGGGGAGAGATGAGGCGTTAAAT	243
Db	432	GGGTGTGGGGGTGGGGGGGTGGGTGGGGGGGTGGGGGGGTGGGGGGGGGGGGGGGG	491
QY	244	TTGCGCATGCTAAACAAGATAGAGAAGGGGAAAAGGCACTATGTTATATTTTAT	303

[illegible]

LOCUS	CV31848	602 bp	mRNA	linear	EST 03-SEP-2004
DEFINITION	LBP09604 Populus stem seasonal library Populus deltoides cDNA, mRNA sequence.				
ACCESSION	CV31848				
VERSION	CV31848.1	GI:51875768			
KEYWORDS	EST.				
SOURCE	Populus deltoides				
ORGANISM	Populus deltoides				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.				
AUTHORS	1 (bases 1 to 602)				
TITLE	Park, S. and Han, K.-H.				
JOURNAL	Gene expression profile during seasonal growth cycle in poplar tree				
COMMENT	Unpublished (2003)				
	Contact: Kyung-Hwan Han				
	Department of Forestry				
	Michigan State University				
	126 Natural Resources, East Lansing, MI 48824-1222, USA				
	Tel: 517 353 4751				
	Fax: 517 432 1143				
	Email: hanhy@msu.edu.				
FEATURES	Location/Qualifiers				
source	1..602				
	/organism="Populus deltoides"				
	/mol_type="mRNA"				
	/strain="IL-129"				
	/db_xref="taxon:3696"				
	/tissue_type="stem"				
	/dev_stage="1 year old"				
	/clone_lib="Populus stem seasonal library"				
ORIGIN					
Query Match	10.0%; Score 45.6; DB 7; Length 602;				
Best Local Similarity	47.9%; Pred. No. 0.43; Mismatches 174; Indels 2; Gaps 1;				
Matches 162; Conservative 0;					
40	TTTTTGTCTCGGTCTCGATCTTTGACCTTGTAGTTTGGTGAGAGCGGCTTCG	99			
DB	368	TTTCCCTTTGGGGGGGGAATTTGGGAGGGGGGTTGGGGGGCTTTTGTGTTT	309		
QY	100	TGCGCCAGANTCGTGCGCGGAGGGGCGGAGATTCTCGCGGCTCTCCGGCGTAGT	159		
DB	308	TCCCCCCCCGGGAGAAAGGGGGGGGGGGCGACAGGGGGTTTAAAGGGGGGAGACGGCCGGGGT	249		
QY	160	CGGCGCCGANTCTCGCGGGAATGGGCTCTCGGATCTGATCTGATCCGCGTGTGG	219		
DB	248	TTTCCCGCCCGGGGGGAAAGGGGGGGCGGAGATGGTAT--TCGGCCCCCTTGG	191		
QY	220	GGGAGATGATGGGGCGTTTAAATTTGCGCATGCTTAAACAGATCAGGAAAGGGGAAA	279		
DB	190	GGGGGATGGGGGCTCCCCGGGGGGGGGGCGGCTTTTGAAGGTTTGGGGGGGGGGG	131		
QY	280	GGGCACTATGGTTTATATTTTATATATATTTCTGCTGCTCGTCAGGCTTGAATGTCT	339		
DB	130	GGGGGGCAGGTTT	71		
QY	340	AGATCTTCTTCTTTTGTGGGAGAAATTGAAT	377		
DB	70	TTTTTTTTTTTTTTTTTTTTTTTTTTTAAATAATAAT	33		

Search completed: September 12, 2005, 03:55:35

Job time : 1199.88 secs

Oy 61 TTWTGGCCCTGGTAGTTGGTAGGGGGAAGCGGCTTCTCGCCGCAAGATCGGTGCGCGG 120
 Db 61 CTTTGACCCTTGGTAGTTTGGTAGTGGGCGAAGCGCGCTTCTCGCCGCAAGATCGGTGCGCGG 120
 Oy 121 AGGGGCGGAGATCTCGCGGCGTGGCGTCTCCGGGCGTGAATCGGCGCGGATCTTCGCGGGGA 180
 Db 121 AGGGGCGGAGATCTCGCGGCGTGGCGTCTCCGGGCGTGAATCGGCGCGGATCTTCGCGGGGA 180
 Oy 181 ATGGGGCTCTCGGAGTGAATCTGAATCCGCGCTGTGTGGGGGAGATGATGGGCGCTTTAA 240
 Db 181 ATGGGGCTCTCGGAGTGAATCTGAATCCGCGCTGTGTGGGGGAGATGATGGGCGCTTTAA 240
 Oy 241 AATTTCGCATCTAAACCAAGATCAGAGAAGGGGAAAAAGGCGCATATGGTTATATTTT 300
 Db 241 AATTTCGCATCTAAACCAAGATCAGAGAAGGGGAAAAAGGCGCATATGGTTATATTTT 300
 Oy 301 TATATATTTCTGCTGCTGCTGCTCAGGCTTAGATGTGTAGATCTTCTCTTCTCTTTT 360
 Db 301 TATATATTTCTGCTGCTGCTGCTCAGGCTTAGATGTGTAGATCTTCTCTTCTCTTTT 360
 Oy 361 GTGGGTAGAATTGGAATCCCTCAGCAATTGTTCATCGGTAGTTTTTCTTTTCAAGATTTGT 420
 Db 361 GTGGGTAGAATTGGAATCCCTCAGCAATTGTTCATCGGTAGTTTTTCTTTTCAAGATTTGT 420
 Oy 421 GACAAATGCAAGCTCGTGGGAGACTTTTGTGAG 454
 Db 421 GACAAATGCAAGCTCGTGGGAGACTTTTGTGAG 454

RESULT 2
US-09-037-531-3
; Sequence 3, Application US/09037531

```

1 GENERAL INFORMATION:
2
3 APPLICANT: DeRose, Richard
4
5 APPLICANT: Freysaet, Georges
6
7 TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
8
9 TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
10
11 TITLE OF INVENTION: And Transformed Plant
12
13 NUMBER OF SEQUENCES: 5
14
15 CORRESPONDENCE ADDRESS:
16
17 ADDRESSER: Connolly, Bove, Lodge, & Hutz
18
19 STREET: 1220 Market Street
20
21 CITY: Wilmington
22
23 STATE: DE
24
25 COUNTRY: USA
26
27 ZIP: 19899
28
29 COMPUTER READABLE FORM:
30
31 MEDIUM TYPE: Floppy disk
32
33 COMPUTER: IBM PC compatible
34
35 OPERATING SYSTEM: PC-DOS/MS-DOS
36
37 SOFTWARE: Patentin Release #1.0, Version #1.25
38
39 CURRENT APPLICATION DATA:
40
41 APPLICATION NUMBER: US/09/037,531
42
43 FILING DATE: 10-MAR-1998
44
45 CLASSIFICATION: 800
46
47 ATTORNEY/AGENT INFORMATION:
48
49 NAME: McMorrow Jr., Robert G.
50
51 REGISTRATION NUMBER: 30962
52
53 REFERENCE/DOCKET NUMBER: 5500*24
54
55 TELECOMMUNICATION INFORMATION:
56
57 TELEPHONE: (302)658-9141
58
59 INFORMATION FOR SEQ ID NO: 3:
60
61 SEQUENCE CHARACTERISTICS:
62
63 LENGTH: 1565 base pairs
64
65 TYPE: nucleic acid
66
67 STRANDEDNESS: single
68
69 TOPOLOGY: linear
70
71 MOLECULE TYPE: DNA (genomic)
72
73 US-09-037-531-3

```

	Matches	454	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	1	GTAAACACCCCGCCCGCCCTCTCTCTTTTCTTTTCTCGATTTTTTTTTTTCGCTCGAGTCTGCAT	60							
Db	1102	GTAAACACCCCGCCCGCCCTCTCTCTTTTCTTTTCTCGATTTTTTTTTTTCGCTCGAGTCTGCAT	116							
QY	61	CTTTGAGCTTTGTAGTTTGAGTGGAGTGGAGAGAGCGGCTTTGTCGCCAGATCGAGTGGCGGG	120							
Db	1162	CTTTGAGCTTTGTAGTTTGAGTGGAGTGGAGAGAGCGGCTTTGTCGCCAGATCGAGTGGCGGG	1222							
QY	121	AGGGGCGGGAGTCTTCGGCGGCTGAGCGCTCTCCGGGCGGTAGTGGGCCCGGATCTCTGGCGGGGA	180							
Db	1222	AGGGGCGGGAGTCTTCGGCGGCTGAGCGCTCTCCGGGCGGTAGTGGGCCCGGATCTCTGGGGGA	128							
QY	181	ATGGGGGCTCTCGAGTGTAGATCTTGATCCGCGGTGTTGGGGGAGATGATGGGGCGTTTAA	240							
Db	1282	ATGGGGGCTCTCGAGTGTAGATCTTGATCCGCGGTGTTGGGGGAGATGATGGGGCGTTTAA	134							
QY	241	AATTTGGCCATGCTAAACAAGATCAGAGACAGGGGAAAAAGGCCACTATAGTTTAAATTTT	300							
Db	1342	AATTTGGCCATGCTAAACAAGATCAGAGACAGGGGAAAAAGGCCACTATAGTTTAAATTTT	140							
QY	301	TATATATTTTCGCTGCTGCTGCTGTCAGGCTTAGATGTGTCTAGATCATCTTTCTTTCTTTT	360							
Db	1402	TATATATTTTCGCTGCTGCTGCTGTCAGGCTTAGATGTGTCTAGATCATCTTTCTTTCTTTT	146							
QY	361	GTGGGTAGAAATTTGAATTCCTCAGACATGTTTCATCGTAGTTTTCCTTTTCATGATTTGT	420							
Db	1462	GTGGGTAGAAATTTGAATTCCTCAGACATGTTTCATCGTAGTTTTCCTTTTCATGATTTGT	152							
QY	421	GACAAATGCAAGCCTCGTGGCGGAGCTTTTGTAG	454							
Db	1522	GACAAATGCAAGCCTCGTGGCGGAGCTTTTGTAG	155							

QY 421 GACAAATGACGCCCTCGTGGCGAGCTTTTGTAG 454
DB 1522 GACAAATGACGCCCTCGTGGCGAGCTTTTGTAG 1555

```

1      RESULT 3
2      US-09-078-862-5
3      : Sequence 5, Application US/09078662
4      : Patent No. 6091003
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Nan, Guo-ling
9      : APPLICANT: Nagai, Chifumi
10     :
11     : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC
12     : TITLE OF INVENTION: TRANSFORMATION OF PINAPPLE
13     :
14     : NUMBER OF SEQUENCES: 6
15     :
16     : CORRESPONDENCE ADDRESS:
17     : ADDRESSEE: Medlen & Carroll, LLP
18     : STREET: 220 Montgomery Street, Suite 2200
19     : CITY: San Francisco
20     : STATE: California
21     : COUNTRY: United States of America
22     :
23     : ZIP: 94104
24     :
25     : COMPUTER READABLE FORM:
26     : MEDIUM TYPE: Floppy disk
27     : COMPUTER: IBM PC compatible
28     : OPERATING SYSTEM: PC-DOS/MS-DOS
29     : SOFTWARE: PatentIn Release #1.0, Version #1.30
30     :
31     : CURRENT APPLICATION DATA:
32     : APPLICATION NUMBER: US/09/078,862
33     : FILING DATE: 14-MAY-1998
34     : CLASSIFICATION: 800
35     :
36     : ATTORNEY/AGENT INFORMATION:
37     : NAME: Carroll, Peter G.
38     : REGISTRATION NUMBER: 32,837
39     :
40     : REFERENCE/DOCKET NUMBER: UH-03321
41     :
42     : TELECOMMUNICATION INFORMATION:
43     : TELEPHONE: (415) 705-8410
44     : TELEFAX: (415) 397-8338
45     :
46     : INFORMATION FOR SEQ ID NO: 5:
47     :
48     : SEQUENCE CHARACTERISTICS:
49     :
50     : LENGTH: 623 base pairs
51     : TYPE: nucleic acid
52     : STRANDEDNESS: double
53     :

```



```

; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/144,602B
;   FILING DATE: 27-OCT-1993
;   CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;     NAME: TIMIAN, SUSAN J.
;     REGISTRATION NUMBER: 34,103
;   REFERENCE/DOCKET NUMBER: 19603/10140
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 716-263-1636
;     TELEFAX: 716-263-1600
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 5643 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;
; US-08-144-602B-4
;
Query Match      83.6%; Score 379.4; DB 1; Length 5643;
Best Local Similarity 93.5%; Pred. No. 5e-105;
Matches 420; Conservative 0; Mismatches 21; Indels 8; Gaps 2;

QY      6  CACCCGCGCCCTCCCTCTTCTTCCGCTTTTTCGTCGCTCCGATCTTTG 65
DB      1736 CCCCAGCCTCCCTCCCTCTTCTTCTTCCGCTTTTTCGTCGCTCCGATCTTTG 1795

QY      66  GCCTTGGTAGTTGGGTGGGCGAGAGCGGCTTCGTCGCCAGATCGGTGGCGGAGAGGG 125
DB      1796 GCCTTGGTAGTTGGGGGCGAGAG-GCGGCTTCGTCGCCAGATCGGTGGCGGAGAGGG 1854

QY      126 CGGAGATTCGGCGGTGGCGGTCTCCGGGCGTGAATCGGCCCGGATCTTCGGGGGATGGG 185
DB      1855 CGGAGATTCGGCGGTGG-----GTCTCGGCGTGGCGGCGGATCTTCGGGGGATGGG 1907

QY      186 GCTCTCGAGTAGTATCTGATCCGCGGTGTGGGGGAGATGATGGGGCGTTAAATTT 245
DB      1908 GCTCTCGAGTAGTATCTGATCCGCGGTGTGGGGGAGATGATGGGGCGTTAAATTT 1967

QY      246 CGCCATCTAAACAAGATCAAGAGAGAGGAGAAAGGCACTATGTTATATTTTATAT 305
DB      1968 CGCCATCTAAACAAGATCAAGAGAGAGGAGAAAGGCACTATGTTATATTTTATAT 2027

QY      306 ATTTCTGCTGCTGCTGCTCAAGCTTAAGATGTCTAGATCTTTCTTTCTTTTGTGGG 365
DB      2028 ATTTCTGCTGCTGCTGCTCAAGCTTAAGATGTCTAGATCTTTCTTTCTTTTGTGGG 2087

QY      366 TAGAATTGGAATCCTCTAGAGATTTGTATCGGTAGTTTCTTTTCAATGATTTGTGCAA 425
DB      2088 TAGAATTGGAATCCTCTAGAGATTTGTATCGGTAGTTTCTTTTCAATGATTTGTGCAA 2147

QY      426 ATGACAGCTCGTGGCGAGCTTTTGTGTAG 454
DB      2148 ATGACAGCTCGTGGCGAGCTTTTGTGTAG 2176

;
; RESULT 8
; US-09-377-466B-19
; Sequence 19, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
;   APPLICANT: Romano, Charles P.
;   TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
;   FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
;   CURRENT APPLICATION NUMBER: US/09/377,466B
;   CURRENT FILING DATE: 1999-08-19
;   NUMBER OF SEQ ID NOS: 43

```

```

; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: expression
;   OTHER INFORMATION: cassette
;   NAME/KEY: promoter
;     LOCATION: (14)..(235)
;   OTHER INFORMATION: P-CamV.AS4
;   NAME/KEY: 5' UTR
;     LOCATION: (240)..(304)
;   OTHER INFORMATION: L-Ta.hcb1
;   NAME/KEY: (intron)
;     LOCATION: (318)..(805)
;   OTHER INFORMATION: I-Os.Act1
;   NAME/KEY: CDS
;     LOCATION: (811)..(2769)
;   OTHER INFORMATION: Cry3Bb1 variant 11231mw1
;   NAME/KEY: terminator
;     LOCATION: (2787)..(3020)
;   OTHER INFORMATION: T-Ta.hep17
;
; US-09-377-466B-19
;
Query Match      78.4%; Score 355.8; DB 4; Length 3039;
Best Local Similarity 92.9%; Pred. No. 5.6e-98;
Matches 430; Conservative 0; Mismatches 22; Indels 11; Gaps 5;

QY      1  GTAACACCCCGCCCTCCCTCTTCTTCCGTTTTCGTTTTCGTCGCTCGAT 60
DB      334  GTAACACCCCGCCCTCCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 393

QY      61  CTTTGGCTTGGTAGTTGGGTGGGCGAGA----GGGCTTCGTCGCCAGATCGGTGGG 116
DB      394  CTTTGGCTTGGTAGTTGGGTGGGCGAGA--GGGCTTCGTCGCCAGATCGGTGGG 453

QY      117 CGGAGAGGGCGGATCTCGCGGTGGCGTCTCGG--GGGTGAGTGGCCCCGGATCTCG 174
DB      454  CGGAGAGGGCGGATCTCGCGGTGGCGTCTCGCGGTGGATCGGCCCGGATCTCG 513

QY      175 CGGGAGATGGGGCTCTCGATGTAGATCT--GATCCGCGTTGTTGGGGAGATGATGGG 232
DB      514  CGGGAGATGGGGCTCTCGATGTAGATCTCGATCCGCGTTGTTGGGGAGATGATGGG 573

QY      233 GCCTTTAAATTT--CGCAGTCTAAACAAGATCAGAGAGGAGAAAGGCACTATGGT 291
DB      574  GCGTTTAAATTTCCGCGCGTCTAAACAAGATCAGAGAGGAGAAAGGCACTATGGT 633

QY      292 TTATATTTTATATATTTTCTGCTGCTGCTGCTGCTGATGATGCTATCTTTCTTT 351
DB      634  TTATATTTTATATATTTTCTGCTGCT--TCGTCAGGCTTAGATGCTATCTTTCTTT 691

QY      352 CTTCTTTTGTGGGTGAATTTGAATCCCTCAGCATTTGTCATCGGTAGTTTCTTTTC 411
DB      692  CTTCTTTTGTGGGTGAATTTGAATCCCTCAGCATTTGTCATCGGTAGTTTCTTTTC 751

QY      412 ATGATTGTGACAAATGACAGCTCTGTCGAGAGCTTTTGTGTAG 454
DB      752  ATGATTGTGACAAATGACAGCTCTGTCGAGAGCTTTTGTGTAG 794

;
; RESULT 9
; US-09-377-466B-21
; Sequence 21, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
;   APPLICANT: Romano, Charles P.
;   TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
;   FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
;   CURRENT APPLICATION NUMBER: US/09/377,466B
;   CURRENT FILING DATE: 1999-08-19
;   NUMBER OF SEQ ID NOS: 43

```

```
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 3039
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: expression
/ OTHER INFORMATION: cassette
/ NAME/KEY: promoter
/ LOCATION: (14)..(235)
/ OTHER INFORMATION: P-CamV.AS4
/ NAME/KEY: 5' UTR
/ LOCATION: (240)..(304)
/ OTHER INFORMATION: L-Ta.hcb1
/ NAME/KEY: Intron
/ LOCATION: (318)..(805)
/ OTHER INFORMATION: I-Os.Act1
/ NAME/KEY: CDS
/ LOCATION: (811)..(2769)
/ OTHER INFORMATION: Cry3Bb1 variant 11231mv2
/ NAME/KEY: terminator
/ LOCATION: (2787)..(3020)
/ OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-21
```

```
Query Match          78.4%; Score 355.8; DB 4; Length 3039;
Best Local Similarity 92.9%; Pred. No. 5.6e-98;
Matches 430; Conservative 0; Mismatches 22; Indels 11; Gaps 5;
```

```
QY 1 GTAAACACCCCGCCCTCTCTCTTTCTTTCCTGTTTTTTTTTTCGTCTCGATCGAT 60
DB 334 GTAACACCCCGCCCTCTCTCTTTCTTTCCTGTTTTTTTTTTCGTCTCGATCGAT 393
QY 61 CTTTGCCCTTGTAAGTTTGGGTGGCGAGA----GCGCTTCGTCGCCGAGTCGGTGGC 116
DB 394 CTTTGCCCTTGTAAGTTTGGGTGGCGAGA--GCGCTTCGTCGCCGAGTCGGTGGC 453
QY 117 CCGGAGGGGCGGAGATCTCGGCGCTGGCGCTCCG--GCGGTGAGTCGCCCGAGTCCTCG 174
DB 454 CCGGAGGGGCGGAGATCTCGGCGCTGGCGCTCCG--GCGGTGAGTCGCCCGAGTCCTCG 513
QY 175 CCGGGAATGGGCTCTCGATGTAGATCT--GATCCGCGCTTGTGGGGAGATGATGGG 232
DB 514 CCGGGAATGGGCTCTCGATGTAGATCTCGATCCGCGTGTGGGGAGATGATGGG 573
QY 233 GCGTTTAAATTT--CGCAGTCTTAAACAAGATCAGGAAGGGGAAAGGGCACTATGGT 291
DB 574 GGGTTTAAATTTCCGCGCTTAAACAAGATCAGGAAGGGGAAAGGGCACTATGGT 633
QY 292 TTATATTTTATATATTTTGTGCTGCTGCTGTCAGGCTTAGATGCTAGATCTTTCTTT 351
DB 634 TTATATTTTATATATTTTGTGCTGCTGCT--TGTGACGGCTTAGATGCTAGATCTTTCTTT 691
QY 352 CTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTTGTCATCGTAGTCTTTCTTTTC 411
DB 692 CTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTTGTCATCGTAGTCTTTCTTTTC 751
QY 412 ATGATTTTGACAATGCAAGCTCGTCCGAGAGCTTTTGTAG 454
DB 752 ATGATTTTGACAATGCAAGCTCGTCCGAGAGCTTTTGTAG 794
```

```
RESULT 10
US-09-377-466B-38
/ Sequence 38, Application US/09377466B
/ Patent No. 6501009
/ GENERAL INFORMATION:
/ APPLICANT: Romano, Charles P.
/ TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
/ FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
/ CURRENT APPLICATION NUMBER: US/09/377,466B
/ CURRENT FILING DATE: 1999-08-19
/ NUMBER OF SEQ ID NOS: 43
```

```
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 38
/ LENGTH: 3044
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: expression
/ OTHER INFORMATION: cassette
/ NAME/KEY: promoter
/ LOCATION: (14)..(235)
/ OTHER INFORMATION: P-CamV.AS4
/ NAME/KEY: 5' UTR
/ LOCATION: (240)..(304)
/ OTHER INFORMATION: L-Ta.hcb1
/ NAME/KEY: Intron
/ LOCATION: (318)..(805)
/ OTHER INFORMATION: I-Os.Act1
/ NAME/KEY: CDS
/ LOCATION: (811)..(2769)
/ OTHER INFORMATION: variant Cry3Bb1 coding sequence encoding v11231
/ NAME/KEY: terminator
/ LOCATION: (2792)..(3025)
/ OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-38
```

```
Query Match          78.4%; Score 355.8; DB 4; Length 3044;
Best Local Similarity 92.9%; Pred. No. 5.6e-98;
Matches 430; Conservative 0; Mismatches 22; Indels 11; Gaps 5;
```

```
QY 1 GTAAACACCCCGCCCTCTCTCTTTCTTTCCTGTTTTTTTTTTCGTCTCGATCGAT 60
DB 334 GTAACACCCCGCCCTCTCTCTTTCTTTCCTGTTTTTTTTTTCGTCTCGATCGAT 393
QY 61 CTTTGCCCTTGTAAGTTTGGGTGGCGAGA----GCGCTTCGTCGCCGAGTCGGTGGC 116
DB 394 CTTTGCCCTTGTAAGTTTGGGTGGCGAGA--GCGCTTCGTCGCCGAGTCGGTGGC 453
QY 117 CCGGAGGGGCGGAGATCTCGGCGCTGGCGCTCCG--GCGGTGAGTCGCCCGAGTCCTCG 174
DB 454 CCGGAGGGGCGGAGATCTCGGCGCTGGCGCTCCG--GCGGTGAGTCGCCCGAGTCCTCG 513
QY 175 CCGGGAATGGGCTCTCGATGTAGATCT--GATCCGCGCTTGTGGGGAGATGATGGG 232
DB 514 CCGGGAATGGGCTCTCGATGTAGATCTCGATCCGCGTGTGGGGAGATGATGGG 573
QY 233 GCGTTTAAATTT--GCGCATGCTTAAACAAGATCAGGAAGGGGAAAGGGCACTATGGT 291
DB 574 GGGTTTAAATTTCCGCGCTTAAACAAGATCAGGAAGGGGAAAGGGCACTATGGT 633
QY 292 TTATATTTTATATATTTTGTGCTGCTGCTGTCAGGCTTAGATGCTAGATCTTTCTTT 351
DB 634 TTATATTTTATATATTTTGTGCTGCTGCT--TGTGACGGCTTAGATGCTAGATCTTTCTTT 691
QY 352 CTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTTGTCATCGTAGTCTTTCTTTTC 411
DB 692 CTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTTGTCATCGTAGTCTTTCTTTTC 751
QY 412 ATGATTTTGACAATGCAAGCTCGTCCGAGAGCTTTTGTAG 454
DB 752 ATGATTTTGACAATGCAAGCTCGTCCGAGAGCTTTTGTAG 794
```

```
RESULT 11
US-09-377-466B-17
/ Sequence 17, Application US/09377466B
/ Patent No. 6501009
/ GENERAL INFORMATION:
/ APPLICANT: Romano, Charles P.
/ TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
/ FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
/ CURRENT APPLICATION NUMBER: US/09/377,466B
/ CURRENT FILING DATE: 1999-08-19
/ NUMBER OF SEQ ID NOS: 43
```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 3450
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: promoter
; LOCATION: (14)..(235)
; OTHER INFORMATION: P-CaMV_354
; NAME/KEY: 5' UTR
; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Os.Act1
; NAME/KEY: transit_peptide
; LOCATION: (825)..(971)
; OTHER INFORMATION: amino terminal TS-Zm.rbcs
; NAME/KEY: intron
; LOCATION: (972)..(1134)
; OTHER INFORMATION: I-Zm.rbcs
; NAME/KEY: transit_peptide
; LOCATION: (1135)..(1221)
; OTHER INFORMATION: carboxy terminus TS-Zm.rbcs
; NAME/KEY: CDS
; LOCATION: (1222)..(3180)
; OTHER INFORMATION: Cry3Bb1 variant 11231mv1
; NAME/KEY: terminator
; LOCATION: (3198)..(3431)
; OTHER INFORMATION: T-Ta.hep17
; JS-09-377-466B-17

```

Query Match	78.4%	Score 355.8	DB 4	Length 3450
Best Local Similarity	92.9%	Pred. No. 6e-98		
Matches 430, Conservative	0	Mismatches 22	Indels 11	Gaps 5

[illegible]

175 CCGGGATGGGGCTTCGGATGATCT - GATCCGCCGTTGTTGGGGGAGATATGGG 23

203 GCGTTTAAAAATT-CCGCATGCTTAAACAGATCAGGAAGAGGGGAAAAGGGCACTATGGT 29

[illegible]

634 TATAATAATTCGCTGCT--TCGACAGGCTAGATGAGTATCTTCTT 63
 635 TTTCTTTTGGGTAGATTTGAATCCCTCAGCATTTGTCATCGGTAGTTTCTTTTC 41

412 ATGATTGTGACCAATGACGCTCGTGCGAGCTTTTGTAG 454
 |||||
 412 ATGATTGTGACCAATGACGCTCGTGCGAGCTTTTGTAG 454
 |||||

RESULT 12
US-09-377-466B-36

Sequence 36, Application US/0937746B8
Patent No. 6501009
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Ab Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Ab Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,46B8
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36

```

? TYPE: DNA
? ORGANISM: Artificial Sequence
FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: expression
? OTHER INFORMATION: cassette
? NAME/KEY: promoter
? LOCATION: (14)..(235)
? OTHER INFORMATION: P. CamV.A54
? NAME/KEY: 5'UTR
? LOCATION: (240)..(304)

```

1	LOCATION: (318)..(805)	
2	OTHER INFORMATION: I-Os,Act1	
3	NAME/KEY: transe1.peptide	
4	LOCATION: (625)..(971)	
5	OTHER INFORMATION: TS-Zm.rbcs amino terminal coding sequence upstream	
6	OTHER INFORMATION: of Zea mays rbcs intron	
7	NAME/KEY: Intron	
8	LOCATION: (972)..(1134)	
9	OTHER INFORMATION: I-Zm.rbcs	

```
LOCATION: (1135)..(1221)
OTHER INFORMATION: TS-Zm.rbcs carboxy terminus coding sequence
OTHER INFORMATION: downstream of Zea mays rbcs intron
```

```

? LOCATION: (1222)..(3180)
? OTHER INFORMATION: variant Cry3Bb1 coding sequence encoding v11231
? NAME/KEY: terminator
? LOCATION: (3198)..(3431)
? OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-36

Query Match          78.4%   Score 355.8; DB 4; Length 3455;
Query Local Similarity 92.9%   Pred. No. 6e-98;
Matches 430; Conservative 0; Mismatches 22; Indels 11; Gaps 5;

```

QY	1	GTAACCAAGCCCGGCGCTCCTCTTTCCTTTCTGTTCGGTCTGGCTGCAT	60
Db	334	GTAACCAAGCCCGGCGCTCCTCTTTCCTTTCTGTTCGGTCTGGCTGCAT	393

61 CTTTGGCCTTGGTAGTTTGGGTGGCCAGA----GCGGCTTGCTGCCCCAGATCGGTGG 116
QY
Db 394 CTTTGGCCTTGGTAGTTTGGGTGGCCAGAGGCGGCTTGTGCGCGCCAGATCGGTGG 453

QY 117 CCGGAGGGGGCGGATCTCCGGCTGGCGCTCTCCG--GGCGTAGTCCGCGCCCGGATCCTTCG 174
Db 454 CCGGAGGGGGCGGATCTCCGGCTGGCGCTCTCCGCGCGTGGATCCGCCCCCGGATCTTCG 513

Qy 175 CCGGGGAATGGGGCTCTCGAGATGTAGATCT--GATCCGCGCTTGTTTGGGGGAATGATGGG 232

Db 514 CCGGGGAATGGGGCTCTCGAGATGTAGATCTCGATCCGCGCTTGTTTGGGGGAATGATGGG 573

QY 233 GCGTTTAAATTT-CGCCATGCTAACAAGATCAGGAAGGGGAAAAAGGCATAATCGT 291

Ddb 574 GGGTTTTAAATTTCGCGCGTGCTAACAAGATCAGAAGGGGAAAAAGGCCTATATGT 633

Db 634 TTATATTTTATATATTTCTGCTGCT--TCGTCAGGCTTAGATGCTAGATCTTTCCTT 631

Qy	35	CTCTTTTGTGGGTGAATTGAAACCTCCTAGACATGTGATCGGTGTTTCTTTC	411
Db	692	CTTCTTTTGTGGGTGAATTGAAACCTCCTAGACATGTGATCGGTGTTTCTTTC	751
Qy	412	ATGATTTTGACAAATGACAGCTCGTGGGAGCTTTTGTG	454
Db	752	ATGATTTTGACAAATGACAGCTCGTGGGAGCTTTTGTG	794

RESULT 13

```

US-09-377-466B-23
: Sequence 23. Application US/09377466B
: Patent No. 6501009
: GENERAL INFORMATION:
: APPLICANT: Romano, Charles P.
: TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
: FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
: CURRENT APPLICATION NUMBER: US/09/377,466B
: CURRENT FILING DATE: 1999-08-19
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 23
: LENGTH: 3469
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: expression
: NAME/KEY: promoter
: LOCATION: (25)..(640)
: OTHER INFORMATION: P-CanV.35S
: NAME/KEY: 5'UTR
: LOCATION: (664)..(734)
: OTHER INFORMATION: L-Ta.hcb1
: NAME/KEY: intron
: LOCATION: (748)..(1238)
: OTHER INFORMATION: I-Os.Act1
: NAME/KEY: CDS
: LOCATION: (1241)..(3199)
: OTHER INFORMATION: Cry3Bb1 variant 11231mv2
: NAME/KEY: terminator
: LOCATION: (3217)..(3450)
: OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-23

```

Query Match	78.4%;	Score 355.8;	DB 4;	Length 3469;
Best Local Similarity	92.9%;	Pred. No. 6e-98;		
Matches 430; Conservative	0;	Mismatches 22;	Indels 11;	Gaps 5;

Oy	1	GTAAACACCCCGCCCTCTCCCTCTTCTCTTCTCCGGTTTTTTTTTTCGTCTGGCTCCGAT	60
Db	764	GTAAACACCCCGCCCTCTCCCTCTTCTCTTCTCCGGTTTTTTTTTTCGTCTGGCTCCGAT	823
Oy	61	CTTTGGCCCTTGGTAGTTTGGGAGGGCGAGA----GGGGCTTCGAGCCAGATCGGTGCG	116
Db	824	CTTTGGCCCTTGGTAGTTTGGGAGGGCGAGAGCGGGCTTCGTGCGGCCAGATCGGTGCG	883
Oy	117	CGGGAGGGGCGGGAGTCTCGCGGCTCGGCTTCG--GGCGTAGTCGGCCCGGATCTTCG	174
Db	884	CGGGAGGGGCGGGAGTCTCGCGGCTTCGCGCGGCGTAGTCGGCCCGGATCTTCG	943
Oy	175	CGGGAGATGGGGCTCTCGAGTAGTAGATCT--GATCCGCGCTGTGTGGGGGAGATAGTGG	232
Db	944	CGGGAGATGGGGCTCTCGAGTAGTAGATCTCGCGATTCGCCGTTGTTGGGGGAGATAGTGG	1003
Oy	233	GGCTTTAAATTT--CGCATGCTAAACAAGATCAGAGAAAGGGGAAAAAGGCATATGCT	291
Db	1004	GGCTTTAAATTTTCGCGCTGCTAAACAAGATCAGAGAAAGGGGAAAAAGGCATATGCT	1063
Oy	292	TTATATTTTTATATATTTCTGCTGCTGCTCGTCAGGCTTAAGATGTCATCTTCTTT	351
Db	1064	TTATATTTTTATATATTTCTGCTGCT--TCGTCAGGCTTAAGATGTCATGCTTCTTT	1121

[illegible]

RESULT 14

```

US-09-068-101-5
: Sequence 5, Application US/09068101
: Patent No. 6372960
: GENERAL INFORMATION:
: APPLICANT: PLANT GENETIC SYSTEMS N.V.
: TITLE OF INVENTION: Improved Barstar Gene
: FILE REFERENCE: 2121-139P
: CURRENT APPLICATION NUMBER: US/09/068,101
: CURRENT FILING DATE: 1998-08-26
: EARLIER APPLICATION NUMBER: EP 96202446.9
: EARLIER FILING DATE: 1996-09-03
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 4032
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: other nucleic
: OTHER INFORMATION: acid, "plasmid pmv71"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1993)..(3400)
: OTHER INFORMATION: label = PRAC1, "promoter region of rice actin gene"
: OTHER INFORMATION: - contains an intron in the leader"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (3401)..(3676)
: OTHER INFORMATION: label = barstar, "barstar DNA"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (3677)..(4003)
: OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
: OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
: OTHER INFORMATION: T-DNA"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (3393)..(3404)
: OTHER INFORMATION: label = NcoI, "NcoI recognition site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (4016)..(4021)
: OTHER INFORMATION: label = KpnI, "KpnI recognition site"
US-09-068-101-5

```

Query Match	76.7%;	Score 348;	DB 3;	Length 4032;
Best Local Similarity	93.1%;	Pred. No. 1.6e-95;		
Matches 432;	Conservative 0;	Mismatches 20;	Indels 12;	Gaps 6

QY	1	GTAAACACCCCGCCCTCTCCCTCTTCTCTTCGCTTTTTTTTTT--CGTTCGCGTCTGA	59
Db	2932	GTAAACACCCCGCCCTCTCCCTCTTCTCTTCGCTTTTTTTTTTTCGCTTCGCTCTGA	299
QY	60	TCCTTGGCCTTGTAATTGGGTGGCGCAGA---GCGGCTTCGTCCGCCAGATCGGTCC	115
Db	2992	TCCTTGGCCTTGTAATTGGGTGGCGCAGAGCGGCTTCGTCCGCCGCCAATCGGTCC	305
QY	116	GCGGGAGGGGGGGGATCTCGCGGCTGGCGGTCTCG--GGCGGATCGCGGCCGGAATCCCTC	173
Db	3052	GCGGGAGGGGGGGGATCTCGCGGCTGGGGGCTCTCGCCGGCGGATCCGGCCCCGATCTC	311
QY	174	GCGGGGAATGGGGCTCTCGATGTGATCT--GATCGCCGTTGTTGGGGGAGATGATGCG	231


```
Db 3112 GCGGGGAATGGGCTCTCGGATGATCTGCGATCCGCCGTTGTTGGGGAGATGATG 3171
QY 232 GCGCTTTAAATTT-GGCCATGCTAAACAAGATCAGAGAAGGGGAAAAGGCACTATG 290
Db 3172 GGGGTTTAAATTTCCGCCATGCTAAACAAGATCAGAGAAGGGGAAAAGGCACTATG 3231
QY 291 TTTATATTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
Db 3232 TTTATATTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3289
QY 351 TCTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATGTTGATCGGTATGTTTCTTT 410
Db 3290 TCTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATGTTGATCGGTATGTTTCTTT 3349
QY 411 CATGATTTGTACAATGACAGCTCTGTGCGGAGCTTTTGTGAG 454
Db 3350 CATGATTTGTACAATGACAGCTCTGTGCGGAGCTTTTGTGAG 3393
```

```
RESULT 15
US-09-970-921-5
; Sequence 5, Application US/09970921
; Patent No. 6759575
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "Plasmid pmv71"
; NAME/KEY: misc feature
; LOCATION: (1995)..(3400)
; OTHER INFORMATION: label = PRACL, "promoter region of rice actin gene
; OTHER INFORMATION: - contains an intron in the leader"
; NAME/KEY: misc feature
; LOCATION: (3401)..(3676)
; OTHER INFORMATION: label = barstar, "barstar DNA"
; NAME/KEY: misc feature
; LOCATION: (3677)..(4003)
; OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
; NAME/KEY: misc feature
; LOCATION: (3395)..(3404)
; OTHER INFORMATION: label = NcoI, "NcoI recognition site"
; NAME/KEY: misc feature
; LOCATION: (4016)..(4021)
; OTHER INFORMATION: label = KpnI, "KpnI recognition site"
US-09-970-921-5
```

```
Query Match 76.7% Score 348; DB 4; Length 4032;
Best Local Similarity 93.1%; Pred. NO. 1.6e-95;
Matches 432; Conservative 0; Mismatches 20; Indels 12; Gaps 6;
```

```
QY 1 GTAACACCCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 59
Db 2932 GTAACACCCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2991
QY 60 TCTTTGGCTTGTAGATTTTGGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 115
Db 2992 TCTTTGGCTTGTAGATTTTGGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3051
QY 116 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 173
Db 3052 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3111
```

```
QY 174 GCGGGGAATGGGCTCTCGGATGATCT--GATCCGCCGTTGTTGGGGAGATGATG 231
Db 3112 GCGGGGAATGGGCTCTCGGATGATCTGCGATCCGCCGTTGTTGGGGAGATGATG 3171
QY 232 GCGCTTTAAATTT-GGCCATGCTAAACAAGATCAGAGAAGGGGAAAAGGCACTATG 290
Db 3172 GGGGTTTAAATTTCCGCCATGCTAAACAAGATCAGAGAAGGGGAAAAGGCACTATG 3231
QY 291 TTTATATTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
Db 3232 TTTATATTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3289
QY 351 TCTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATGTTGATCGGTATGTTTCTTT 410
Db 3290 TCTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATGTTGATCGGTATGTTTCTTT 3349
QY 411 CATGATTTGTACAATGACAGCTCTGTGCGGAGCTTTTGTGAG 454
Db 3350 CATGATTTGTACAATGACAGCTCTGTGCGGAGCTTTTGTGAG 3393
```

Search completed: September 12, 2005, 04:00:33
Job time : 75.0862 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: September 12, 2005, 02:27:12 ; Search time 578.125 Seconds
(without alignments)
5157.238 Million cell updates/sec

Title: US-10-758-799-2

Sequence: 1 GATACACCCCGCCCTCTC.....CGTGGAGCTTTTGTGAG 454

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	100.0	454	9	US-09-037-531-2
2	454	100.0	454	19	US-10-758-799-2
3	454	100.0	1565	9	US-09-037-531-3
4	454	100.0	1565	19	US-10-758-799-3
5	382.2	84.2	470	16	US-10-087-167-109
6	379.4	83.6	623	9	US-09-981-900B-19
7	357.4	78.7	9359	21	US-10-344-977A-1

8	357.4	78.7	9359	22	US-10-344-975B-1	Sequence 1, Appli
9	355.8	78.4	491	9	US-09-376-940-50	Sequence 50, Appl
10	355.8	78.4	1597	22	US-10-839-092-50	Sequence 50, Appl
11	355.8	78.4	3034	20	US-10-841-796-34	Sequence 34, Appl
12	355.8	78.4	3039	15	US-10-232-665-19	Sequence 19, Appl
13	355.8	78.4	3039	15	US-10-232-665-21	Sequence 21, Appl
14	355.8	78.4	3044	15	US-10-232-665-18	Sequence 38, Appl
15	355.8	78.4	3450	15	US-10-232-665-17	Sequence 17, Appl
16	355.8	78.4	3455	15	US-10-232-665-36	Sequence 36, Appl
17	355.8	78.4	3469	15	US-10-232-665-23	Sequence 23, Appl
18	355.8	78.4	7794	24	US-11-057-062-2	Sequence 2, Appli
19	355.8	78.4	8590	20	US-11-057-062-1	Sequence 1, Appli
20	355.8	78.4	11546	20	US-10-841-796-33	Sequence 33, Appli
21	348	76.7	1384	22	US-10-839-092-35	Sequence 35, Appl
22	348	76.7	2480	21	US-10-678-588A-1	Sequence 1, Appli
23	348	76.7	4032	9	US-09-970-921-5	Sequence 5, Appli
24	348	76.7	5365	22	US-10-839-092-57	Sequence 57, Appl
25	348	76.7	6865	10	US-09-845-064-13	Sequence 13, Appl
26	348	76.7	7943	10	US-09-845-064-15	Sequence 15, Appl
27	348	76.7	9143	10	US-09-845-064-12	Sequence 12, Appl
28	348	76.7	10003	10	US-09-845-064-21	Sequence 21, Appl
29	348	76.7	10003	10	US-09-845-064-21	Sequence 21, Appl
30	346.4	76.3	4176	24	US-11-004-221-7	Sequence 7, Appli
31	338.4	74.5	2378	15	US-10-213-791-27	Sequence 27, Appl
32	338.4	74.5	8296	24	US-11-057-069-1	Sequence 1, Appli
33	290.2	63.9	2107	15	US-10-213-791-29	Sequence 29, Appl
34	290.2	63.9	2122	15	US-10-213-791-35	Sequence 25, Appl
35	203	44.7	1259	10	US-09-991-209-33	Sequence 43, Appl
36	203	44.7	4773	10	US-09-991-209-32	Sequence 32, Appl
37	203	44.7	4950	10	US-09-991-209-34	Sequence 34, Appl
38	203	44.7	4965	10	US-09-991-209-37	Sequence 37, Appl
39	203	44.7	4974	10	US-09-991-209-35	Sequence 35, Appl
40	203	44.7	5164	10	US-09-991-209-36	Sequence 36, Appl
41	203	44.7	5277	10	US-09-991-209-35	Sequence 25, Appl
42	203	44.7	5295	10	US-09-991-209-38	Sequence 38, Appl
43	203	44.7	5327	10	US-09-991-209-27	Sequence 27, Appl
44	203	44.7	5337	10	US-09-991-209-19	Sequence 19, Appl
45	203	44.7	5337	10	US-09-991-209-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-037-531-2
; Sequence 2, Application US/09037531
; Patent No. US20020104117A1
GENERAL INFORMATION:
APPLICANT: Derose, Richard
TITLE OF INVENTION: Freysinet, Georges
TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
TITLE OF INVENTION: And Transformed Plant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,531
FILING DATE: 10-MAR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McMorrow Jr., Robert G.
REGISTRATION NUMBER: 30962


```

1 ORGANISM: Artificial Sequence
2 FEATURE:
3 OTHER INFORMATION: Vector pVDH636 nucleotide sequence
4 FEATURE:
5 NAME/KEY: gene
6 LOCATION: (839)..(1699)
7 OTHER INFORMATION: Beta-lactamase gene (Ampr)
8 FEATURE:
9 NAME/KEY: gene
10 LOCATION: (4921)..(6400)
11 OTHER INFORMATION: AclH1 gene from Arabidopsis thaliana
12 FEATURE:
13 NAME/KEY: polyA_signal
14 LOCATION: (6401)..(6672)
15 OTHER INFORMATION: Poly-A signal from the nopaline synthetase gene from Agrobacterium
16 FEATURE:
17 NAME/KEY: polyA_signal
18 LOCATION: (9120)..(9359)
19 OTHER INFORMATION:
20 FEATURE:
21 NAME/KEY: misc_feature
22 LOCATION: (7434)..(8084)
23 OTHER INFORMATION: First exon-intron combination from Ubi-maize
24 FEATURE:
25 NAME/KEY: gene
26 LOCATION: (8085)..(9119)
27 OTHER INFORMATION: Hygromycin resistance gene from Escherichia coli
28 FEATURE:
29 NAME/KEY: promoter
30 LOCATION: (12941)..(4920)
31 OTHER INFORMATION: Ubi-promoter from maize
32 US-10-344-977A-1

```


OTHER IN
FEATURE:

```

; SOFTWARE: E
; SEQ ID NO 21

```

```

1 LENGTH: 3039
2 TYPE: DNA
3 ORGANISM: Artificial Sequence
4 FEATURE:
5 OTHER INFORMATION: Description of Artificial Sequence: expression
6 OTHER INFORMATION: cassette
7 FEATURE:
8 NAME/KEY: Promoter
9 LOCATION: (14)..(235)
10 OTHER INFORMATION: P-CaMV.AS4
11 FEATURE:
12 NAME/KEY: 5'UTR
13 LOCATION: (240)..(304)
14 OTHER INFORMATION: L-Ta.hcb1
15 FEATURE:
16 NAME/KEY: Intron
17 LOCATION: (318)..(805)
18 OTHER INFORMATION: I-Os.Act1
19 FEATURE:
20 NAME/KEY: CDS
21 LOCATION: (811)..(2769)
22 OTHER INFORMATION: Cry3Bb1 variant 11231mw2
23 FEATURE:
24 NAME/KEY: terminator
25 LOCATION: (2787)..(3020)
26 OTHER INFORMATION: T-Ta.hsp17
27 US-10-232-665-21

```

Query Match	78.4%;	Score 355.8;	DB 15;	Length 3039;
Best Local Similarity	92.9%;	Pred. No. 7e-96;		
Matches 430; Conservative	0;	Mismatches 22;	Indels 11;	Gaps 5;

OY	1	GTAAACCAACCCGCCCCCTCCCTCTCTTCTCTTCTCCGATTTTTTTTTTTTTTTCGCTCGATCTCGAT	60
Dd	334	GTAAACCAACCCGCCCCCTCCCTCTCTTCTCTTCTCTCCGATTTTTTTTTTTTTTTCGCTCGATCTCGAT	393
OY	61	CTTTGACCTTGATGTTTGAGTGAGGCGAGA----CGAGCTTCGTGCGCCAGATCGGTGCG	116
Dd	394	CTTTGACCTTGATGTTTGAGTGAGGCGAGAGAGCGAGCTTCGTGCGGCCAGATCGGTGCG	453
OY	117	CGGAGAGGGCGCGGATCTCGCGGCTTGGCGTCTCCG--GGCGTAGTCGGCCCGGATCTCTCG	174
Dd	454	CGGAGAGGGCGCGGATCTCGCGGCTTGGCGGCTTCGCGCGCGATGAGATCGGACCGGATCTCG	513
OY	175	CGGGGAATGGGAGCTCTCGAGATGATGATCT--GATCCGCGCTTGTTGGGGAGATGATGCGG	232
Dd	514	CGGGGAATGGGAGCTCTCGAGATGATGATCTCGAGATCTCGCGCTTGTTGGGGAGATGATGCGG	573
OY	233	CGGTTTAAATTT--CGCCATGCTTAAACAAGATCAGAGAGGGGAAAGGCGCATGATGCT	291
Dd	574	CGGTTTAAATTTTCGCGCGTGTCTTAAACAAGATCAGAGAGGGGAAAGGCGCATGATGCT	633
OY	292	TTATATTTTTTANATTTCTGCTGCTCGCTCGCAGAGCTTAAATGATGCTAGATCTTCTT	351
Dd	634	TTATATTTTTTANATTTCTGCTGCT--TCGCAAGAGCTTAAATGCTAGATCTTCTT	691
OY	352	CTTCTTTTGTGGAGATTTGAATTCCTCAGACATTGTTCACTCGATGATTTTTCTTTTC	411
Dd	692	CTTCTTTTGTGGAGATTTGAATTCCTCAGACATTGTTCACTCGATGATTTTTCTTTTC	751
OY	412	ATGATTTGTGCAAAATGACGCTCTGTGCGAGCTTTTTTTTGG	454
Dd	752	ATGATTTGTGCAAAATGACGCTCTGTGCGAGCTTTTTTTTGG	794

```

RESULT 14
US-10-232-665-38
; Sequence 38, Application US/10232665
; Publication No. US20030115630A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15104) Cry3Bb Improved Exp. Corn

```

```

1 CURRENT APPLICATION NUMBER: US/10/232,665
2 CURRENT FILING DATE: 2002-08-29
3 PRIOR APPLICATION NUMBER: US/09/377,466
4 PRIOR FILING DATE: 1999-08-19
5 NUMBER OF SEQ ID NOS: 43
6 SOFTWARE: PatentIn Ver. 2.0
7 SEQ ID NO 38
8 LENGTH: 3044
9 TYPE: DNA
10 ORGANISM: Artificial Sequence
11 FEATURE:
12 OTHER INFORMATION: Description of Artificial Sequence: expression
13 OTHER INFORMATION: cassette
14 FEATURE:
15 NAME/KEY: promoter
16 LOCATION: (14)..(235)
17 OTHER INFORMATION: P-CMV.AS4
18 FEATURE:
19 NAME/KEY: 5'UTR
20 LOCATION: (240)..(304)
21 OTHER INFORMATION: L-Ta.hcb1
22 FEATURE:
23 NAME/KEY: intron
24 LOCATION: (318)..(805)
25 OTHER INFORMATION: I-Os.Act1
26 FEATURE:
27 NAME/KEY: CDS
28 LOCATION: (811)..(2769)
29 OTHER INFORMATION: variant Cry3Bb1 coding sequence encoding vll231
30 FEATURE:
31 NAME/KEY: terminator
32 LOCATION: (2792)..(3025)
33 OTHER INFORMATION: T-Ta.hsp17
34 US-10-232-665-38

```

Query Match	78.4%;	Score 355.8;	DB 15;	Length 3044;
Best Local Similarity	92.9%;	Pred. No. 7e-96;		
Matches 430;	Conservative	0;	Mismatches 22;	Indels 11;
				Gaps 5

QY	1	GTAAACACACCCGCCCTCTCCCTCTTTCTTTTCGCGATTTTTCCTGCTCGATCGAT	60
Db	334	GTAAACACACCCGCCCTCTCTCTTTCTTTTCCTCGTTTTCCTCGCTCGATCGAT	393
QY	61	CTTTGGCCTTGTAAGTTTGGGTGGGCGAGA---GCGGCTTTCGTGCCCAATCGGTGCG	116
Db	394	CTTTGGCCTTGTAAGTTTGGGTGGGCGAGAGGCGGCTTTCGTGGCGGCCCAATCGGTGCG	453
QY	117	CGGAGAGGGGCGGGATCTCGCGGCTGGCGCTTCGG---GGGTGAGTCCGGCCCGGATCCGCG	174
Db	454	CGGAGAGGGGCGGGATCTCGCGGCTGGCGGCTTCGGCGGCGTGAATCCGAGCCCGGATCTCG	513
QY	175	CGGGGAATGAGGGCTCTCGAGTGTAGATCT--GATCCGCGCTGTGTGGGGGAGATAGTGGG	232
Db	514	CGGGGAATGAGGGCTCTCGAGTGTAGATCTGGGATTCGCGCTGTGTGGGGGAGATAGTGGG	573
QY	233	GCGTTTAAAAATTT--CGCCATGCTAAACAAGATCAGAGAGAGGGGAAAAAGGCGACTATGCT	291
Db	574	GCGTTTAAAAATTTCCGCGCTCTAAACAAGATCAGAGAGAGGGGAAAAAGGCGACTATGCT	633
QY	252	TTAATATTTTATATATTTCTGCTGCTGCTCGTCAAGCTTAATATGTGATAGATCTTTTCCTT	351
Db	634	TTAATATTTTATATATTTCTGCTGCT--TCGTCAAGCTTAATATGTGATAGATCTTTTCCTT	691
QY	352	CTTCTTTTGGGGGAGATTTGAATCCCTCAGCATTTTTCATCGGTATGTTTCTTTTC	411
Db	692	CTTCTTTTGGGGGAGATTTGAATCCCTCAGCATTTTTCATCGGTATGTTTCTTTTC	751
QY	412	ATGATTTTGTGCAAAATGAGCGCTCGTGGAGCTTTTTCGAG	454
Db	752	ATGATTTTGTGCAAAATGAGCGCTCGTGGAGCTTTTTCGAG	794

RESULT 15


```

Db      181  ATGGGCTCTCGAGTATGATCTGATCCGCTGTGTGGGGAGATGATGGGCGTTTAA 240
QY      241  AATTGGCATGCTAAACAAGATCAGGAGAGGGGAAAGGACATAGGTTATATTT 300
Db      241  AATTGGCATGCTAAACAAGATCAGGAGAGGGGAAAGGACATAGGTTATATTT 300
QY      301  TATATATTTCTGCTGCTGCTCGTCAAGGCTTAGATGAGTCTAGATCTTCTTCTTTT 360
Db      301  TATATATTTCTGCTGCTGCTCGTCAAGGCTTAGATGAGTCTAGATCTTCTTCTTTT 360
QY      361  GTGGGAGAGATTTGAATCCCTCAGCATTTTCAATCGGTAGTTTCTTTTCAATGATTGT 420
Db      361  GTGGGAGAGATTTGAATCCCTCAGCATTTTCAATCGGTAGTTTCTTTTCAATGATTGT 420
QY      421  GACAAATGACGCTCGTGGGAGCTTTTGTAG 454
Db      421  GACAAATGACGCTCGTGGGAGCTTTTGTAG 454

RESULT 2
AR559744
LOCUS      AR559744
DEFINITION Sequence 2 from patent US 6750378.
ACCESSION AR559744
VERSION    AR559744.1 GI:53969842
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 454)
AUTHORS   Deroee,R. and Freysinet,G.
TITLES    Maize H3c4 promoter combined with the first intron of rice actin,
           chimeric gene comprising it and transformed plant
JOURNAL    Patent: US 6750378-A 2 15-JUN-2004;
FEATURES   Location/Qualifiers
            source
              1..454
              /organism="unknown"
              /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 454; DB 6; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.8e-246;
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTAACACCCCGCCCTCTCTCTTCTTCTCGGTTTTTTTGGTCTCGGCTCGAT 60
Db      1  GTAACACCCCGCCCTCTCTCTTCTTCTCGGTTTTTTTGGTCTCGGCTCGAT 60
QY      61  CTTTGGCTTGTAGTTGGGTGGGCGAGACGGCTTCTGCGCCAGATCGGTGCGGG 120
Db      61  CTTTGGCTTGTAGTTGGGTGGGCGAGACGGCTTCTGCGCCAGATCGGTGCGGG 120
QY      121  AGGGGCGGGATCTCGCGGCTGGGCTCTCGGGGCTGAGTGGCCCGGATCTTGGCGGG 180
Db      121  AGGGGCGGGATCTCGCGGCTGGGCTCTCGGGGCTGAGTGGCCCGGATCTTGGCGGG 180
QY      121  AGGGGCGGGATCTCGCGGCTGGGCTCTCGGGGCTGAGTGGCCCGGATCTTGGCGGG 180
Db      121  AGGGGCGGGATCTCGCGGCTGGGCTCTCGGGGCTGAGTGGCCCGGATCTTGGCGGG 180
QY      181  ATGGGCTCTCGGATGATGATCTGATCCGCGTTTGGGGAGATGAGGGGCTTTAA 240
Db      181  ATGGGCTCTCGGATGATGATCTGATCCGCGTTTGGGGAGATGAGGGGCTTTAA 240
QY      181  ATGGGCTCTCGGATGATGATCTGATCCGCGTTTGGGGAGATGAGGGGCTTTAA 240
Db      181  ATGGGCTCTCGGATGATGATCTGATCCGCGTTTGGGGAGATGAGGGGCTTTAA 240
QY      241  AATTGGCATGCTAAACAAGATCAGGAGAGGGGAAAGGACATAGGTTATATTT 300
Db      241  AATTGGCATGCTAAACAAGATCAGGAGAGGGGAAAGGACATAGGTTATATTT 300
QY      301  TATATATTTCTGCTGCTGCTCGTCAAGGCTTAGATGAGTCTAGATCTTCTTCTTTT 360
Db      301  TATATATTTCTGCTGCTGCTCGTCAAGGCTTAGATGAGTCTAGATCTTCTTCTTTT 360
QY      361  GTGGGAGAGATTTGAATCCCTCAGCATTTTCAATCGGTAGTTTCTTTTCAATGATTGT 420
Db      361  GTGGGAGAGATTTGAATCCCTCAGCATTTTCAATCGGTAGTTTCTTTTCAATGATTGT 420
QY      421  GACAAATGACGCTCGTGGGAGCTTTTGTAG 454
Db      421  GACAAATGACGCTCGTGGGAGCTTTTGTAG 454

```

```

Db      421  GACAAATGACGCTCGTGGGAGCTTTTGTAG 454

RESULT 3
BD128390
LOCUS      BD128390
DEFINITION BD128390 454 bp DNA linear PAT 18-SEP-2002
           Corn H3c4 promoter bonded to the first intron of rice actin,
           chimeric gene containing this promoter and transgenic plant.
ACCESSION BD128390.1 GI:23223335
VERSION    JP 200250016-A/2.
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 454)
AUTHORS   Duroee,R. and Freysinet,G.
TITLES    Corn H3c4 promoter bonded to the first intron of rice actin,
           chimeric gene containing this promoter and transgenic plant
JOURNAL    Patent: JP 200250016-A 2 08-JAN-2002;
FEATURES   AVENTIS CROPS SCIENCE SA
            OS Unidentified
            PN JP 200250016-A/2
            PD 08-JAN-2002
            PF 22-DEC-1998 JP 2000526660
            PR 24-DEC-1997 FR 97/16726
            PI RICHARD DUROEE, GEORGES FREYSINET
            PC C12N15/09,A01H5/00,C07K14/21,C07K14/415,C07K19/00,C12N5/10, PC
            C12Q1/68
            CC C12N15/00,C12N5/00
            CC Strandedness: Single;
            CC Topology: Linear;
            CC Corn H3c4 promoter bonded to the first intron of rice actin,
            CC containing this promoter and transgenic plant FH Key
            CC Location/Qualifiers
            FT source
              1..454
              /organism='Unidentified'.
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"

ORIGIN
Query Match      100.0%; Score 454; DB 6; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.8e-246;
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTAACACCCCGCCCTCTCTCTTCTTCTCGGTTTTTTTGGTCTCGGCTCGAT 60
Db      1  GTAACACCCCGCCCTCTCTCTTCTTCTCGGTTTTTTTGGTCTCGGCTCGAT 60
QY      61  CTTTGGCTTGTAGTTGGGTGGGCGAGACGGCTTCTGCGCCAGATCGGTGCGGG 120
Db      61  CTTTGGCTTGTAGTTGGGTGGGCGAGACGGCTTCTGCGCCAGATCGGTGCGGG 120
QY      61  CTTTGGCTTGTAGTTGGGTGGGCGAGACGGCTTCTGCGCCAGATCGGTGCGGG 120
Db      61  CTTTGGCTTGTAGTTGGGTGGGCGAGACGGCTTCTGCGCCAGATCGGTGCGGG 120
QY      121  AGGGGCGGGATCTCGCGGCTGGGCTCTCGGGGCTGAGTGGCCCGGATCTTGGCGGG 180
Db      121  AGGGGCGGGATCTCGCGGCTGGGCTCTCGGGGCTGAGTGGCCCGGATCTTGGCGGG 180
QY      121  AGGGGCGGGATCTCGCGGCTGGGCTCTCGGGGCTGAGTGGCCCGGATCTTGGCGGG 180
Db      121  AGGGGCGGGATCTCGCGGCTGGGCTCTCGGGGCTGAGTGGCCCGGATCTTGGCGGG 180
QY      181  ATGGGCTCTCGGATGATGATCTGATCCGCGTTTGGGGAGATGAGGGGCTTTAA 240
Db      181  ATGGGCTCTCGGATGATGATCTGATCCGCGTTTGGGGAGATGAGGGGCTTTAA 240
QY      181  ATGGGCTCTCGGATGATGATCTGATCCGCGTTTGGGGAGATGAGGGGCTTTAA 240
Db      181  ATGGGCTCTCGGATGATGATCTGATCCGCGTTTGGGGAGATGAGGGGCTTTAA 240
QY      241  AATTGGCATGCTAAACAAGATCAGGAGAGGGGAAAGGACATAGGTTATATTT 300
Db      241  AATTGGCATGCTAAACAAGATCAGGAGAGGGGAAAGGACATAGGTTATATTT 300
QY      301  TATATATTTCTGCTGCTGCTCGTCAAGGCTTAGATGAGTCTAGATCTTCTTCTTTT 360
Db      301  TATATATTTCTGCTGCTGCTCGTCAAGGCTTAGATGAGTCTAGATCTTCTTCTTTT 360

```

LOCUS	AR559745	1565 bp	DNA	linear	PAT 08-OCT-2004
DEFINITION	Sequence 3 from patent US 6750378.				
ACCESSION	AR559745				
VERSION	AR559745.1	GI:53969843			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1565)				
TITLE	Derose,R. and Freysinet,G.				
JOURNAL	Maize H3c4 promoter combined with the first intron of rice actin,				
FEATURES	chimeric gene comprising it and transformed plant				
SOURCE	Patent: US 6750378-A 3 15-JUN-2004;				
	Location/Qualifiers				
	1..1565				
	/organism="unknown"				
	/mol_type="genomic DNA"				
ORIGIN					
Query Match	100.0%;	Score 454;	DB 6;	Length 1565;	
Best Local Similarity	100.0%;	Pred. No. 1.9e-246;			
Matches 454;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	GTAACACACCCGGCCCTCTCCTCTTTTCTCTCGTTTCTTTTCTGCTCGGCTCGAT	60		
Db	1102	GTAACACACCCGGCCCTCTCCTCTTTTCTCGTTTCTGTTTCTGTTTCTGAT	1161		
QY	61	CTTTGGCTTGTAATTTGGGTGGCGAGACGGCTTCGTGCCAGATCGTGGCGGG	120		
Db	1162	CTTTGGCTTGTAATTTGGGTGGCGAGACGGCTTCGTGCCAGATCGTGGCGGG	1221		
QY	121	AGGGCGGGATCTTCGGCGGTGGCGTCTCCGGCGGTGAGTCGGCCCGATCCTCGCGGGA	180		
Db	1222	AGGGCGGGATCTTCGGCGGTGGCGTCTCCGGCGGTGAGTCGGCCCGATCCTCGCGGGA	1281		
QY	181	ATGGGCGTCTCCGATGTGATCTGATTCGCGCGTTTGGGGAGATGATGGCGGCTTAA	240		
Db	1282	ATGGGCGTCTCCGATGTGATCTGATTCGCGCGTTTGGGGAGATGATGGCGGCTTAA	1341		
QY	241	AATTTGCGCATGTCAAACAAGATCAGGAGAGGGGAAAAGGCACTATGGTTTATTTT	300		
Db	1342	AATTTGCGCATGTCAAACAAGATCAGGAGAGGGGAAAAGGCACTATGGTTTATTTT	1401		
QY	301	TATATATTTTGTGCTGCTGCTGTCTCAGGCTTAGATGTGCTAGATCTTTCTTTCT	360		
Db	1402	TATATATTTTGTGCTGCTGCTGTCTCAGGCTTAGATGTGCTAGATCTTTCTTTCT	1461		
QY	361	GTGGGTGAATTTGAATTCCTCAGCATTTTCATCGGTAGTTTCTTTTCATGATTTGT	420		
Db	1462	GTGGGTGAATTTGAATTCCTCAGCATTTTCATCGGTAGTTTCTTTTCATGATTTGT	1521		
QY	421	GACAAATGCAGCCCTCGGGGAGGATTTTTGTAG	454		
Db	1522	GACAAATGCAGCCCTCGGGGAGGATTTTTGTAG	1555		
RESULT 6					
LOCUS	BD128391	1565 bp	DNA	linear	PAT 18-SEP-2002
DEFINITION	Corn H3c4 promoter bonded to the first intron of rice actin,				
ACCESSION	BD128391				
VERSION	BD128391.1	GI:23223336			
KEYWORDS	JP 2002500016-A/3.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 1565)				
AUTHORS	Durose,R. and Freysinet,G.				
TITLE	Corn H3c4 promoter bonded to the first intron of rice actin,				
JOURNAL	chimeric gene containing this promoter and transgenic plant				
	Patent: JP 200250016-A 3 08-JAN-2002;				
	AVENTIS CROSCIENCE SA				

COMMENT	OS	Unidentified
	PN	JP 2002500016-A/3
	PD	08-JAN-2002
	PF	22-DEC-1998 JP 2000526660
	PR	24-DEC-1997 FR 97/16726
	PI	RICHARD DUROSE, GEORGE FREYSIET
	PC	CL1201/68, CL1201/69, A01H5/00, C07K14/21, C07K14/415, C07K19/00, C12N5/10, PC
	PC	CL12N15/00, C12N5/00
	CC	Strandedness: Single;
	CC	Topology: linear;
	CC	Corn H3c4 promoter bonded to the first intron of rice actin,
	CC	chimeric gene
	CC	containing this promoter and transgenic plant FH
	CC	Location/Qualifiers
	FT	1. .1565
	FT	source
		/organism='Unidentified'.
		Location/Qualifiers
		1. .1565
		/organism='unidentified'
		/mol_type='genomic DNA'
		/db_xref='taxon:32644'

Query Match	100.0%	Score 454	DB 6	length 165;
Best Local Similarity	100.0%	Prod. No.	1.9e-246;	
Matches 454;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	1	GTAACGACCAGCCCGCCTCTCCCTCTTTCCTTTTCCTTCGGTTTTTTTTTTCGTCTCGATCAT	60
Dd	1102	GTAACGACCAGCCCGCCTCTCCCTCTTTCCTTCGGTTTTTTTTTTCGTCTCGATCAT	1161
Oy	61	CTTTGGCCTTGGAATTGGTGGGGCGAGAAGCGCTTGTGCGCCAAGATCGGTGGCGGG	120
Dd	1162	CTTTGGCCTTGGAATTGGTGGGGCGAGAAGCGCTTGTGCGCCAAGATCGGTGGCGGG	1221
Oy	121	AGGGGCGGGAAATTCGCGGCTGGCGCTCTCCGGGCGTAGAGTCGGCCCCGGAATCCCTCGCGGGGA	180
Dd	1222	AGGGGCGGGAAATTCGCGGCTGGCGCTCTCCGGGCGTAGAGTCGGCCCCGGAATCCCTCGCGGGGA	1281
Oy	181	ATGGGGCTCTCGAGTGTAGATCTGATCCGCGCTTGTGGGGGAGATGATGGGGCGTTTAA	240
Dd	1282	ATGGGGCTCTCGAGTGTAGATCTGATCCGCGCTTGTGTGGGGGAGATGATGGGGCGTTTAA	1341
Oy	241	AATTTGGCAAGCTTAAACAAGATCGAGAAGAGGGGAAAAGGCAATAATGTTTAAATTT	300
Dd	1342	AATTTGGCAAGCTTAAACAAGATCGAGAAGAGGGGAAAAGGCAATAATGTTTAAATTT	1401
Oy	301	TATATATTTCTGCTCTGCTCGTCAAGGCTTATGATGTGCATATCTTCTCTTCTTTT	360
Dd	1402	TATATATTTCTGCTCTGCTCGTCAAGGCTTATGATGTGCATATCTTCTCTTCTTTT	1461
Oy	361	GTGGGTAGAAATTTGAATCCCTCAGACTTGTTCATCTGGTAGTTTTCCTTTTCATGATTTGT	420
Dd	1462	GTGGGTAGAAATTTGAATCCCTCAGACTTGTTCATCTGGTAGTTTTCCTTTTCATGATTTGT	1521
Oy	421	GACAAATGCAAGCTCTGGCGGAGCTTTTTTTAG	454
Dd	1522	GACAAATGCAAGCTCTGGCGGAGCTTTTTTTAG	1555

RESULT 7				
LOCUS	AX467609			
DEFINITION	Sequence 19 from Patent WO0234926.	623 bp	DNA	linear
ACCESSION	AX467609			
VERSION	AX467609.1	GI:21900797		
KEYWORDS				
SOURCE				
ORGANISM				
	<i>Oryza sativa</i>			
	<i>Oryza sativa</i>			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; <i>Oryza</i> .			

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1	Sticklen, M. B., Dale, B. E. and Magpool, S.	Transgenic plants containing ligninase and cellulase which degrade lignin and cellulose to fermentable sugars	Patent: WO 0234926-A 19 02-MAY-2002; MICHIGAN STATE UNIVERSITY (US)	Location/Qualifiers 1..623 /organism="Oryza sativa" /mol_type="unassigned DNA" /db_xref="taxon:4530"

```
Query Match      64.1%; Score 291; DB 6; Length 623;
Best Local Similarity 100.0%; Pred. NO. 1.le-153;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

[illegible]

RESULT	8			
OSACIT1				
LOCUS	O.sativa	Act1	gene.	
DEFINITION		623 bp	DNA	linear
ACCESSION	X63830			PLN 24-MAR-199
VERSION	X63830.1			
KEYWORDS	act1 gene; actin; Gus gene.			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Oryza sativa (japonica cultivar-group)			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
	Eriarthroideae; Oryzeae; Oryza.			
REFERENCE	1			
AUTHORS	Mcelroy,D., Blowers,A.D., Jones,B. and Wu,R.			
TITLE	Construction of expression vectors based on the rice actin 1 (Act1			
JOURNAL	5' region for use in monocot transformation			
MEDLINE	Mol. Gen. Genet. 231 (1), 150-160 (1991)			
PUBMED	92092956			
REFERENCE	1753941			
AUTHORS	2 (bases 1 to 623)			
TITLE	Wu,R.J.			
JOURNAL	Direct Submission			
	Submitted (21-MAR-1994) R.J. Wu, Cornell University, Section of			
	Biochemistry Molecular & Cell Biology, 316 Biotechnology Building,			
	Ithaca, NY 14853, USA			
FEATURES	Location/Qualifiers			
source	1..623			
	/organism="Oryza sativa (japonica cultivar-group)"			
	/mol_type="genomic DNA"			
	/cultivar="B-42"			
	/sub_species="japonica"			
	/db_xref="taxon:39947"			
	1..8			
	join(42..120,569..623)			
	/gene="Act1"			


```

mRNA
join(42..120,569..>623)
/gene="Act1"
exon
42..120
/gene="Act1"
/number=1
/evidence=experimental
intron
121..568
/gene="Act1"
/number=1
569..>623
/gene="Act1"
/number=2
/evidence=experimental
576..>623
/gene="Act1"
/codon_start=1
/product="actin"
/protein_id="CAA45324.1"
/db_xref="GI:468506"
/db_xref="UniProt/TrEMBL:Q40656"
/translation="MADAPDGSPGQSLM"
621..623
/gene="Gus"
621..>623
/gene="Gus"
/codon_start=1
/protein_id="CAA45325.1"
/db_xref="GI:4379330"
/translation="M"
CDS

```

ORIGIN

Query Match	64.1%;	Score 291;	DB 8;	Length 623;
Best Local Similarity	100.0%;	Pred. No. 1.1e-153;		
Matches 291;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	164	CGGATCTCTCGGGGGAATGGGGCTCTCGGATGTGATCTGATCCGCGTGTGGGGGA	223
Db	278	CGGATCTCTCGGGGGAATGGGGCTCTCGGATGTGATCTGATCCGCGTGTGGGGGA	337
OY	224	GATGATGGGGCGTTTTAAATTTCCGCATGCTAAACAATCAGGAAGGGGAAAAAGGC	283
Db	338	GATGATGGGGCGTTTTAAATTTCCGCATGCTAAACAATCAGGAAGGGGAAAAAGGC	397
OY	284	ACTATGTTTATTTATATATTTCTGCTCTGCTGTCGAGCTTTGATGTGCTAGAT	343
Db	398	ACTATGTTTATTTATTTATATTTCTGCTCTGCTGTCGAGCTTTGATGTGCTAGAT	457
OY	344	CTTTCCTTCTCTTTTGTGGGTAGAAATTTGAAATCCTCAGCAATGTTCAATCGTAGTTT	403
Db	458	CTTTCCTTCTCTTTTGTGGGTAGAAATTTGAAATCCTCAGCAATGTTCAATCGTAGTTT	517
OY	404	TTCTTTTATATTTGTGACAAATGACAGCTGTGCGGAGCTTTTGTAG	454
Db	518	TTCTTTTATATTTGTGACAAATGACAGCTGTGCGGAGCTTTTGTAG	568

LOCUS	150114	1392 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 6 from patent US 5641876.				
ACCESSION	150114				
VERSION	150114.1	GI:2472334			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1392)				
AUTHORS	McElroy,D. and Wu,R.				
TITLE	Rice actin gene and promoter				
JOURNAL	Patent: US 5641876-A 6 24-JUN-1997;				
FEATURES	Location/Qualifiers				
source	1..1392				
	/organism="unknown"				

```
ORIGIN
      /mol_type="unassigned DNA"
```

Query Match	64.1%	Score 291	DB 6	Length 1392
Best Local Similarity	100.0%	Pred. No.	1.1e-153	
Matches 291	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	164	CCGATCCTCCGGGGGAATGGGCGCTCCGAGTGAAGATCTGATCCGCGTGTGGGGGA	223
Db	1076	CCGATCCTCGCGGGGAATGGGCGCTCCGAGTGAAGATCTGATCCGCGTGTGGGGGA	1139
Qy	224	GATGATGGGCGCTTAAATTTCCGCACTGCTAAACAAGATCAGGAAAGGGGAAAAGGCC	283
Db	1136	GATATATGGGCGTTTAAATTTCCCAATGCTAAACAAGATCAGGAAAGGGGAAAAGGCC	1199
Qy	284	ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGTCAGGCTTATGATGCTAGAT	343
Db	1196	ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGTCAGGCTTATGATGCTAGAT	1255
Qy	344	CTTTCCTTCTTCTTTTGTGGGTAAGATTGAATCCTCAGCAATTTGTCATCGGTAGTTT	403
Db	1256	CTTTCCTTCTTCTTTTGTGGGTAAGATTGAATCCTCAGCAATTTGTCATCGGTAGTTT	1319
Qy	404	TTCTTTTCAGATTTTGACAAAGCAAGCCCTCGAGCGGAGCTTTTTTTTAG	454
Db	1316	TTCTTTTCAGATTTTGACAAAGCAAGCCCTCGAGCGGAGCTTTTTTTTAG	1366

RESULT 10

LOCUS	1404 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 7 from patent US 5641876.			

VERSION	IS0115.1	GI:2472335
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 1404)	
TITLE	McElroy,D. and Wu,R.	
JOURNAL	Rice actin gene and promoter	
FEATURES	Parent: US 5641876-A 7 24-JUN-1997;	
source	Location/Qualifiers	
	1..1404	

ORIGIN

Query Match	64.1%;	Score 291;	DB 6;	Length 1404;
Best Local Similarity	100.0%;	Pred. No. 1.1e-153;		
Matches 291;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	16	CCGGAATCTCGCGGGAGAAATGGGAGCTCTCGAATGTAAGATCTGATCCGCGGTGTGGGGGA	223
QY <td>1086</td> <td>CCGGAATCTCGCGGGAGAAATGGGAGCTCTCGAATGTAAGATCTGATCCGCGGTGTGGGGGA</td> <td>1145</td>	1086	CCGGAATCTCGCGGGAGAAATGGGAGCTCTCGAATGTAAGATCTGATCCGCGGTGTGGGGGA	1145
QY <td>224</td> <td>GATGATGCGGGCGTTAAAAATTTGCCCATGCTAAACAAGATCAGGAAGAAGGGAAAGGGC</td> <td>283</td>	224	GATGATGCGGGCGTTAAAAATTTGCCCATGCTAAACAAGATCAGGAAGAAGGGAAAGGGC	283
Db <td>1146</td> <td>GATGATGCGGGCGTTAAAAATTTGCCCATGCTAAACAAGATCAGGAAGAAGGGAAAGGGC</td> <td>1205</td>	1146	GATGATGCGGGCGTTAAAAATTTGCCCATGCTAAACAAGATCAGGAAGAAGGGAAAGGGC	1205
QY <td>284</td> <td>ACATAGGTTATATTTTATATATTTCTGCGCGCTGCTGACGGCTTAGATGTCCTGAT</td> <td>343</td>	284	ACATAGGTTATATTTTATATATTTCTGCGCGCTGCTGACGGCTTAGATGTCCTGAT	343
Db <td>1206</td> <td>ACATAGGTTATATTTTATATATTTCTGCGCGCTGCTGACGGCTTAGATGTCCTGAT</td> <td>1265</td>	1206	ACATAGGTTATATTTTATATATTTCTGCGCGCTGCTGACGGCTTAGATGTCCTGAT	1265
QY <td>344</td> <td>CTTTCCTTCTCTTTTGTGGGAGAAATTTGAATCCCTCAGACATTTTCATCGGTAGTT</td> <td>403</td>	344	CTTTCCTTCTCTTTTGTGGGAGAAATTTGAATCCCTCAGACATTTTCATCGGTAGTT	403
Db <td>1266</td> <td>CTTTCCTTCTCTTTTGTGGGAGAAATTTGAATCCCTCAGACATTTTCATCGGTAGTT</td> <td>1325</td>	1266	CTTTCCTTCTCTTTTGTGGGAGAAATTTGAATCCCTCAGACATTTTCATCGGTAGTT	1325
QY <td>404</td> <td>TTCTTTTCAGATTTTGACAAAGCAGCCCTGCGCGAGAGCTTTTGTAG</td> <td>454</td>	404	TTCTTTTCAGATTTTGACAAAGCAGCCCTGCGCGAGAGCTTTTGTAG	454
Db <td>1326</td> <td>TTCTTTTCAGATTTTGACAAAGCAGCCCTGCGCGAGAGCTTTTGTAG</td> <td>1376</td>	1326	TTCTTTTCAGATTTTGACAAAGCAGCCCTGCGCGAGAGCTTTTGTAG	1376

LOCUS	150113	2199 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 5 from patent US 5641876.				
ACCESSION	150113				
VERSION	150113.1	GI:2472333			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2199)				
AUTHORS	McElroy,D. and Wu,R.				
TITLE	Rice actin gene and promoter				
JOURNAL	Patent: US 5641876-A 5 24-JUN-1997;				
FEATURES	location/Qualifiers				
source	1..2199				
	/organism="unknown"				
	/mol_type="unassigned DNA"				

Query Match	64.1%	Score 291	DB 6	Length 2199
Best Local Similarity	100.0%	Pred. No.	1.2e-153	
Matches 291	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	164	CCGAGTCTCGCGGGAAATGCGGCTCTCGAGTGTAGATCTGATCCGCCGTTGTGGGGA	223	
Db	1883	CCGAGTCTCGCGGGAAATGCGGCTCTCGAGTGTAGATCTGATCCGCCGTTGTGGGGA	1942	
QY	224	GATGATGGGGCGTTAAAAATTCGGCATCGCTAAACAAGTCAGAAAGGGGAAAAAGGC	283	
Db	1943	GATGATGGGGCGTTAAAAATTCGGCATCTTAAACAAGTCAGAAAGGGGAAAAAGGC	2002	
QY	284	ACTATGTTTATATATTTTATATATATTTCTGCTGCTGTCAGGCTTAGATGTCTAAT	343	
Db	2003	ACTATGTTTATATATTTTATATATATTTCTGCTGCTGTCAGGCTTAGATGTCTAAT	2062	
QY	344	CTTTCCTTCTCTTTTGTGGGTAGAAATTGAAATCCCTCAGACATGTTTCATCGTAGT	403	
Db	2063	CTTTCCTTCTCTTTTGTGGGTAGAAATTGAAATCCCTCAGACATGTTTCATCGTAGT	2122	
QY	404	TTCTTTTCATGATTTTGTGACAAATCGAGCTCTGTGCGAGCTTTTGTGAG	454	
Db	2123	TTCTTTTCATGATTTTGTGACAAATCGAGCTCTGTGCGAGCTTTTGTGAG	2173	

RESULT	12			
LOCUS	150112	5643 bp	DNA	linear
DEFINITION	Sequence 4 from patent US 5641876.			
ACCESSION	150112			
VERSION	150112.1	GI:2472332		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 5643)			
TITLE	McElroy, D. and Wu, R.			
JOURNAL	Rice actin gene and promoter			
FEATURES	Patent: US 5641876-A 4 24-JUN-1997;			
	Location/Qualifiers			
	1..5643			
	/organism="Unknown"			
	/mol_type="unassigned DNA"			
ORIGIN				

	Query Match	Similarity	Score	DB	Length
Best Local	100.0%	Pred. No. 1.2e-153			
Matches	291	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0

QY	164	CCGAGTCTCGCGGGGATGGGGCTCTCGAGTGTGATTCGCGCGCTTGTGGGGG	223
Db	1886	CCGAGTCTCTCGGGGGAATGGGGCTCTCGAGTGTGATTCGCGCGCTTGTGGGGG	1945

QY	221	GATATAGGGGGCTTTAAAATTTGGCCATGCTAAACAAGATAGAGAGGGGAAAAGGC	283
Db	1946	GATATAGGGGGGTTAAAATTTCGCCATGCTAAACAAGATAGAGAGGGGAAAAGGC	2005
QY	284	ACTATGGTTATATTTTATATATTTCTGCTGCTCTGTCAGGCTTAGATGTGCTAGAT	343
Db	2006	ACTATGGTTATATTTTATATATTTCTGCTGCTCTGTCAGGCTTAGATGTGCTAGAT	2065
QY	344	CTTTCCTTCTTCTTTTGTGGGTAGAAATTGAAATCCCTCAGCATTTGTCATCGGTAGTTT	403
Db	2066	CTTTCCTTCTTCTTTTGTGGGTAGAAATTGAAATCCCTCAGCATTTGTCATCGGTAGTTT	2125
QY	404	TTCTTTTCATGATTTTGACAAATAGCAGCCTCGTGCGGAGCTTTTGTAG	454
Db	2126	TTCTTTTCATGATTTTGACAAATAGCAGCCTCGTGCGGAGCTTTTGTGTAG	2176

RESULT 13				
LOCUS	AX555357	470 bp	DNA	linear
DEFINITION	Sequence 109 from Patent WO02061102.			
ACCESSION	AX555357			
VERSION	AX555357.1	GI:25898876		
KEYWORDS				
SOURCE				
ORGANISM				
	Oryza sp.			
	Oryza sp.			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
	Ehretoidae; Oryzaceae; Oryza.			
REFERENCE				
AUTHORS	1 Pascual,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.			
TITLE	Control of gene expression in plants			
JOURNAL	Patent: WO 02061102-A 109 08-AUG-2002;			
	Syngenta Participations AG (CH)			
FEATURES				
source	location/Qualifiers			
	1..470			
	/organism="Oryza sp."			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:52841"			

Query Match	63.7%	Score 289	DB 6	Length 470
Best Local Similarity	100.0%	Prod. No. 1.5e-152		
Matches 289	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	166	GGATTCCTGGCGGGGAAATGGGGCTCTCGAGTGAATCTGATCCGCCGCTGTGTTGGGGGAGA	225	
Db	166	GGATTCCTGGCGGGGAAATGGGGCTCTCGAGTGAATCTGATCCGCCGCTGTGTTGGGGGAGA	225	
QY	226	TGATGGGGCGTTTAAATTTGGCCATGTTAAACAAGATCAGAGAGGGGAAAAAGGGCAC	285	
Db	226	TGATGGGGCGTTTAAATTTGGCCATGTTAAACAAGATCAGAGAGGGGAAAAAGGGCAC	285	
QY	286	TATGGTTATATATTTTATATATATTTCTGCTGCTGCTCGTCAAGCTTAAATGTGCTAGATCT	345	
Db	286	TATGGTTATATATTTTATATATATTTCTGCTGCTGCTCGTCAAGCTTAAATGTGCTAGATCT	345	
QY	346	TTCTTTCTCTTTTGGTGGTAGAATTGAATCCCTGACGATTTGTTACGCTAGATTTT	405	
Db	346	TTCTTTCTCTTTTGGTGGTAGAATTGAATCCCTGACGATTTGTTACGCTAGATTTT	405	
QY	406	CTTTTCATGATTTGTGACAAATGACGCTCGTGGGAGCTTTTTTTGAG 454		
Db	406	CTTTTCATGATTTGTGACAAATGACGCTCGTGGGAGCTTTTTTTGAG 454		

RESULT 14			
AX641982		1121 bp	DNA
LOCUS			linear
DEFINITION	Sequence 15 from Patent WO02096192.		
ACCESSION	AX641982		
VERSION	AX641982.1	GI:28474610	
			PAT 21-FEB-2003

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Werner, S., Marillemet, S., Klimuk, V. and Gleba, Y.
TITLE Process of producing environmentally safe transgenic organisms
JOURNAL Patent: WO 02096192-A 15 05-DEC-2002;
Icon Genetics AG (DE)
FEATURES
source
1. .1121
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3' fragment of synthetic CryIIIA gene preceeded by
3' end of rice actin 1 intron flanked by HindIII and BamHI
sites"

ORIGIN
Query Match 45.8%; Score 208; DB 6; Length 1121;
Best Local Similarity 100.0%; Pred. No. 2e-106;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 247 GCCATGCTAAACAAGATCAGAGAGGGGAAAGGGGACATGCTTATATTTTATATA 306
DB 7 GCCATGCTAAACAAGATCAGAGAGGGGAAAGGGGACATGCTTATATTTTATATA 66
QY 307 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
DB 67 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126
QY 367 AGAATTGGAATCCCTCAGCATGTTTCATCGGATGTTTCTTTTCATGATTGTGACAA 426
DB 127 AGAATTGGAATCCCTCAGCATGTTTCATCGGATGTTTCTTTTCATGATTGTGACAA 186
QY 427 TGCAGCTCTGCTGCGGAGCTTTTGTG 454
DB 187 TGCAGCTCTGCTGCGGAGCTTTTGTG 214

RESULT 15
AY452735 4895 bp DNA circular SYN 19-DEC-2003
LOCUS
DEFINITION Reporter vector pActXN, complete sequence.
ACCESSION AY452735
VERSION AY452735.1 GI:39636979
KEYWORDS
SOURCE Reporter vector pActXN
ORGANISM Reporter vector pActXN
REFERENCE other sequences; artificial sequences; vectors.
1 (bases 1 to 4895)
AUTHORS Vickers, C.E., Xue, G.P. and Greshoff, P.M.
TITLE A synthetic xylanase as a novel reporter in plants
JOURNAL Plant Cell Rep. 22 (2), 135-140 (2003)
MEDLINE 22867549
PUBMED 12845475
REFERENCE 2 (bases 1 to 4895)
AUTHORS Vickers, C.E.
TITLE Direct Submision
JOURNAL Submitted (29-OCT-2003) ARC Centre for Integrative Legume Research,
The University of Queensland, Room 213, John Hines Building (69),
St. Lucia, QLD 4072, Australia
FEATURES
source
1. .4895
/organism="Reporter vector pActXN"
/mol_type="other DNA"
/db_xref="taxon:255329"
267. .2274
/note="sequence from cloning vector pBR322"
468. .1328
/note="ampicillin resistance protein; bla"
/codon_start=1
/product="beta-lactamase"

/protein_id="AAR29085.1"
/db_xref="GI:39636980"
/translation="MSIQHFRVALIPFPAFLPLPFAHPETLVKVKDAEDQLAGVGY
ILDILNSGKILSFPRPEEFPMWSTFVKLLCGAVLSRIDAGEQQLRIHISQNDLVE
YSPVTEKHLTDGMTVRELCSAAITWSDNTAAAILITIGGPRELAFILNMGDHVTPL
DSPEELINEAIPNDRSDITPMVAMATYLRKLLTGBLTLASRQQLIDMEADKVGPL
LRSAIPAGFIADKSGAGERSGRIIAALGPDKPSRIYIVITTSQATMDRRNQIA
EIGASLIKHW"
2345. .2367
misc_feature
/note="T7 RNA polymerase promoter"
2426. .3338
promoter
/note="from rice actin gene; Act1"
3339. .3792
intron
/note="intron 1 from rice actin gene; Act1"
3800. .4513
gene
/gene="xynA"
3800. .4513
CDS
/gene="xynA"
/note="synthetic xylanase"
/codon_start=1
/product="Xylanase"
/protein_id="AAR29086.1"
/db_xref="GI:39636981"
/translation="MASNGKFTVGNQGNQHGKGVNDFSEYELMDVTGNGSWTLGSG
ATPKAEWNAAVNRGNPLARGLDPSOKATLDYDGLDVAATYQOTASAGNSRLCV
YGMFQRGLNGVPLVBYITIEDVWVMPDPAQKMTTIDGAKYIKITQMDTPTINGSG
ETFKQYFSVRQKRTSGHTVSDHFREMAKQGMIGNLVYALNAGWOSGVADVTL
LDVYTPPKSSPATSAPR"
4535. .4872
terminator
/note="from rbcS gene"
4895
misc_feature
/note="SP6 RNA polymerase transcription initiation site"

ORIGIN
Query Match 44.9%; Score 204; DB 12; Length 4895;
Best Local Similarity 100.0%; Pred. No. 4.1e-104;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAACACCCCGCCCT 60
DB 3339 GTAACACCCCGCCCT 3398
QY 61 CTTTGCCCTTGGATGTTGGGCGGAGAGCGGCTTCTCGCCCGAGATCGGTGCCGGG 120
DB 3399 CTTTGCCCTTGGATGTTGGGCGGAGAGCGGCTTCTCGCCCGAGATCGGTGCCGGG 3458
QY 121 AGGGGCGGAGATCTCGGCGCTGGGCGTCTCGGGCGGTGAGTCGGCCCGATCTTGGCGGGA 180
DB 3459 AGGGGCGGAGATCTCGGCGCTGGGCGTCTCGGGCGGTGAGTCGGCCCGATCTTGGCGGGA 3518
QY 181 ATGGGCTCTCGGATGATGATCTG 204
DB 3519 ATGGGCTCTCGGATGATGATCTG 3542

Search completed: September 12, 2005, 11:40:50
Job time : 1557.26 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 03:55:48 ; Search time 260.167 Seconds
(Without alignments)
10330.128 Million cell updates/sec

Title: US-10-758-799-2

Perfect score: 454
Sequence: 1 GTAAACCAACCCGCCCTCTC.....CGTGGAGCTTTTGTAG 454

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: Geneseq_16Dec04:*
2: geneseqn19808:*
3: geneseqn19908:*
4: geneseqn20008:*
5: geneseqn2001as:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	100.0	454	AAZ91038	Aaz91038 Rice acti
2	454	100.0	1565	AAZ91039	Aaz91039 ChimERIC
3	291	64.1	623	AAZ47117	Aaz47117 Rice Acti
4	291	64.1	623	ABK86738	ABK86738 Rice Acti
5	291	64.1	1392	AAT80053	Aat80053 Rice acti
6	291	64.1	2199	AAT80052	Aat80052 Rice acti
7	291	64.1	5643	AAT80055	Aat80055 Rice acti
8	289	63.7	470	ABT07357	ABT07357 Reporter
9	289	63.7	470	ADF49181	Adf49181 Rice acti
10	208	45.8	1121	ABZ70926	Abz70926 CytIIIA 3
11	204	44.9	13680	ADP73931	Adp73931 Plasmid p
12	203	44.7	1259	ADG69912	Adg69912 Actin pro
13	203	44.7	1259	ADN88926	Adn88926 Actin pro
14	203	44.7	3657	ADG68992	Adg68992 Vector pr
15	203	44.7	4604	ADG68905	Adg68905 Vector pr
16	203	44.7	4773	ADG69901	Adg69901 Vector pr
17	203	44.7	4773	ADN88915	Adn88915 pGTV vect
18	203	44.7	4950	ADG69903	Adg69903 Vector pr
19	203	44.7	4950	ADN88917	Adn88917 pU06.1 ve
20	203	44.7	4965	ADG69906	Adg69906 Vector pr

ALIGNMENTS

21	203	44.7	4974	6	ADG69904	Adg69904 Vector pr
22	203	44.7	4974	11	ADN88918	Adn88918 pU04 vect
23	203	44.7	5164	11	ADN88919	Adn88919 pP010.1 v
24	203	44.7	5267	11	ADN88907	Adn88907 pTP8-5 ve
25	203	44.7	5277	6	ADG69894	Adg69894 Vector pr
26	203	44.7	5277	11	ADN88909	Adn88909 pTP5-1 ve
27	203	44.7	5295	6	ADG69907	Adg69907 Vector pr
28	203	44.7	5295	11	ADN88922	Adn88922 pU04 vect
29	203	44.7	5327	6	ADG69896	Adg69896 Vector pr
30	203	44.7	5327	11	ADN88911	Adn88911 pTP42 ve
31	203	44.7	5337	6	ADG69888	Adg69888 Vector pr
32	203	44.7	5337	6	ADG69900	Adg69900 Vector pr
33	203	44.7	5337	11	ADN88914	Adn88914 pTP5 vect
34	203	44.7	5337	11	ADN88903	Adn88903 pTP4 vect
35	203	44.7	5338	6	ADG69884	Adg69884 Vector pr
36	203	44.7	5338	6	ADG69898	Adg69898 Vector pr
37	203	44.7	5338	11	ADN88913	Adn88913 pTP3-1 ve
38	203	44.7	5338	11	ADN88899	Adn88899 pTP10-1 v
39	203	44.7	5345	6	ADG69886	Adg69886 Vector pr
40	203	44.7	5345	11	ADN88901	Adn88901 pU04-4 ve
41	203	44.7	5387	6	ADG69910	Adg69910 Vector pr
42	203	44.7	5387	11	ADN88925	Adn88925 pTP1-1 v
43	203	44.7	5395	6	ADG69890	Adg69890 Vector pr
44	203	44.7	5395	11	ADN88905	Adn88905 pTP5.14 v
45	203	44.7	5510	2	AAQ12707	Aaq12707 Rice acti

RESULT 1
AAZ91038 standard; DNA; 454 BP.
ID AAZ91038;
AC AAZ91038;
XX
XX
DT 06-JUN-2000 (first entry)
XX
XX
DE Rice actin gene intron 1 sequence.
XX
XX
KW Regulatory element; monocotyledonous vegetable plant cell; maize;
KW histone H3C4; promoter; rice actin gene intron; chimeric; ss;
KW herbicide resistance.
XX
XX
OS Oryza sativa.
OS
XX
XX
PN FR2772787-A1.
XX
XX
PD 25-JUN-1999.
XX
XX
PF 24-DEC-1997; 97FR-00016726.
XX
XX
PR 24-DEC-1997; 97FR-00016726.
XX
XX
PA (RHON) RHONE-POULENC AGROCHIMIE.
XX
XX
PI Derose R. Freyssiinet G;
XX
XX
DR WPI; 1999-397352/34.
XX
XX
PT 5' chimeric regulatory region comprising maize histone H3C4 promoter and
PT rice actin gene first intron.
XX
XX
PS Claim 5; Page 14; 24pb; French.
XX
XX
CC The invention relates to a DNA sequence (AAZ91039) comprising a 5'
CC regulatory element for the expression of a heterologous gene in a
CC monocotyledonous vegetable plant cell. The DNA comprises: (a) a
CC functional fragment of the maize histone H3C4 promoter sequence
CC (AAZ91037); and (b) a functional fragment of the first intron of the rice
CC actin gene (this sequence). The chimeric regulatory region is useful for
CC the expression of heterologous genes that confer resistance to certain
CC herbicides, or that have novel agronomical properties in monocotyledons.

Query Match	Best Local Similarity	Score	DB	Length					
Matches	291	Conservative	0	Mismatches	0	Indels	0	Gaps	0
164	CCGAGATCTTCGCGGGAATGAGGAGCTTCGAGATGATGATCTGATCCGCGGTTGTTGGGAGA	223							
278	CCGAGATCTTCGCGGGAATGAGGAGCTTCGAGATGATGATCTGATCCGCGGTTGTTGGGAGA	337							

OY	224	GATGATGGGGCGCTTTAAATTTCCGCAATGCTAAACAAATGATCAGAAAGAGGGGAAAAAGCGC	263
Db	338	GATGATGGGGCGCTTTAAATTTCCGCAATGCTAAACAAATGATCAGAAAGAGGGGAAAAAGCGC	397
OY	284	ACTATGGTTATATTTTTTATATTTCTGCGCTGCTGTCAGGCTTAGATGTCAGAT	343
Db	398	ACTATGGTTATATTTTTTATATTTCTGCGCTGCTGTCAGGCTTAGATGTCAGAT	457
OY	344	CTTTCCTTCTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCAATGTTTCATCGGTACGTTT	403
Db	458	CTTTCCTTCTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCAATGTTTCATCGGTACGTTT	517
OY	404	TTCTTTTCATGATTTGTGCAAAATGACGCTCTGTGCGGAGCTTTTTGTAG	454
Db	518	TTCTTTTCATGATTTGTGCAAAATGACGCTCTGTGCGGAGCTTTTTGTAG	568
RESULT 4			
ABK86738	ID	ABK86738 standard; DNA; 623 BP.	
AC	ABK86738;		
XX	24-SEP-2002	(first entry)	
DT			
XX	Rice Act1 gene.		
DE			
XX	Rice; gene; ds; transgenic; plant; lignocellulose; cellulase; ligninase;		
KW	fermentable sugar; ethanol; fermentation; silage; feed; fuel;		
KW	industrial chemical; biodegradation; chloroaromatic;		
KM	environmental pollutant; Act1.		
XX			
OS	Oryza sativa.		
XX			
PN	WO200234926-A2.		
XX			
PD	02-MAY-2002.		
XX			
PF	18-OCT-2001; 2001WO-US032538.		
XX			
PR	20-OCT-2000; 2000US-0242408P.		
XX			
PA	(UNMS) UNIV MICHIGAN STATE.		
XX			
PI	Sticklen MB, Dale BG, Magpool S;		
XX			
DR	WPI; 2002-489947/52.		
XX			
PT	Producing transgenic plants which after harvest degrade lignin and		
PT	cellulose to fermentable sugars, by mating transgenic plant comprising		
PT	DNA encoding cellulase with transgenic plant comprising DNA encoding		
PT	ligninase.		
XX			
PS	Example 1; Page 124; 126pp; English.		
XX			
XX			
CC	The invention discloses the production of a transgenic plant which		
CC	degrades lignocellulose when the plant is ground. It comprises the		
CC	production of the transgenic plant including cellulase and ligninase by		
CC	mating a transgenic plant, containing a DNA encoding a cellulase, and a		
CC	transgenic plant, containing a DNA encoding a ligninase, where both genes		
CC	are operably linked to a nucleotide sequence encoding a signal peptide		
CC	which targets the fusion protein to an organelle of the plant,		
CC	particularly chloroplasts. The method is useful for producing a		
CC	transgenic plant (e.g. maize) which degrades lignocellulose when the		
CC	plant is ground to produce a plant material. This material is useful for		
CC	converting lignocellulose, in a plant material, to fermentable sugars		
CC	which are then fermented to ethanol. The transgenic plants also provide		
CC	plentiful and inexpensive source of fungal or bacterial cellulases and		
CC	ligninases which can be used in the production of ethanol. They can also		
CC	be used for pre-treating silage to increase the energy value of		
CC	lignocellulosic feeds for cows and other ruminant animals, pre-treating		
CC	lignocellulosic biomass for fermentative conversion to fuels and		

XX This sequence represents the promoter region from the rice actin-1 (Rac1) gene. Cytoplasmic actin is a fundamental and essential component of the eukaryotic cell and cytoskeleton. In higher plant cells, a number of cellular processes, such as cytoplasmic streaming, extension growth and cell division are thought to involve the cytoskeletal actin protein. All CC of the studied plant actins consist of four exons of conserved length. CC separated by 3 introns of variable length. In rice there are at least 8 CC actin-like sequences per haploid genome. Rac1 encodes a transcript that CC is relatively abundant in all rice tissues. This sequence is an example CC of a nucleic acid molecule of the invention. The nucleic acid molecules CC of the invention contain the Rac1 gene (or fragments) with promoter CC activity in monocotyledonous plants. The promoter is used to direct CC expression of foreign genes in transgenic rice and other plants. The CC actin promoter is more efficient in rice transformation than previously CC proposed promoters (e.g. 5 times more active than the maize Adh1 CC promoter) and has constitutive activity in space and time. (Updated on 25 CC -MAR-2003 to correct PF field.)

XX Sequence 2199 BP; 603 A; 515 C; 446 G; 635 T; 0 U; 0 Other;

Query Match 64.1%; Score 291; DB 2; Length 2199;

Best Local Similarity 100.0%; Pred. No. 2.1e-130; Mismatches 0; Gaps 0; Matches 291; Conservative 0; Indels 0;

QY 164 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCCGCGTTGTTGGGGGA 223
DB 1883 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCCGCGTTGTTGGGGGA 1942

QY 224 GATGATGGGGCGTTAAATTTGSCATGCTAAACAAGATCAGGAAGGGGAAAAGGGC 283
DB 1943 GATGATGGGGCGTTAAATTTGSCATGCTAAACAAGATCAGGAAGGGGAAAAGGGC 2002

QY 284 ACTATGGTTAAATTTTATATATTTCTGCTGCTGCTCAGGCTTAGATGTGCTAGAT 343
DB 2003 ACTATGGTTAAATTTTATATATTTCTGCTGCTGCTCAGGCTTAGATGTGCTAGAT 2062

QY 344 CTTTCCTTCTCTTTTGTGGGAGAAATTTGAATCCCTCAGACTTGTTCATCGGTAGTTT 403
DB 2063 CTTTCCTTCTCTTTTGTGGGAGAAATTTGAATCCCTCAGACTTGTTCATCGGTAGTTT 2122

QY 404 TTCTTTTCATGATTTTGACAAATGACCTCCGCGGAGCTTTTGTGAG 454
DB 2123 TTCTTTTCATGATTTTGACAAATGACCTCCGCGGAGCTTTTGTGAG 2173

RESULT 7
AAT80055
ID AAT80055 standard; cDNA; 5643 BP.

XX AAT80055;

XX 25-MAR-2003 (revised)
DT 04-NOV-1997 (first entry)

XX Rice actin 1 gene.

XX Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;
KM cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.

XX Oryza sativa.

XX US5641876-A.

XX 24-JUN-1997.

XX 27-OCT-1993; 93US-00144602.

XX 05-JAN-1990; 90US-00461490.

XX 18-SEP-1991; 91US-00762680.

XX (CORR) CORNELL RES FOUND INC.

PI Wu R, Mcelroy D;

XX WPI; 1997-340996/31.

XX Nucleic acid containing the promoter of the rice actin-1 gene - used to

PT direct efficient expression of foreign genes in rice.

PS Example 1; Col 3-7; 29pp; English.

XX This sequence represents a the rice actin-1 (Rac1) gene amplified using CC AAT80054. Cytoplasmic actin is a fundamental and essential component of CC the eukaryotic cell and cytoskeleton. In higher plant cells, a number of CC cellular processes, such as cytoplasmic streaming, extension growth and CC cell division are thought to involve the cytoskeletal actin protein. All CC of the studied plant actins consist of four exons of conserved length, CC separated by 3 introns of variable length. In rice there are at least 8 CC actin-like sequences per haploid genome. Rac1 encodes a transcript that CC is relatively abundant in all rice tissues. This sequence is an example CC of a nucleic acid molecule of the invention. The nucleic acid molecules CC of the invention contain the Rac1 gene, or fragments with promoter CC activity (see AAT80052 and AAT80053) in monocotyledonous plants. The CC promoter is used to direct expression of foreign genes in transgenic rice CC and other plants. The actin promoter is more efficient in rice CC transformation than previously proposed promoters (e.g. 5 times more CC active than the maize Adh1 promoter) and has constitutive activity in CC space and time. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 5643 BP; 1500 A; 1283 C; 1200 G; 1660 T; 0 U; 0 Other;

Query Match 64.1%; Score 291; DB 2; Length 5643;

Best Local Similarity 100.0%; Pred. No. 2.1e-130; Mismatches 0; Gaps 0; Matches 291; Conservative 0; Indels 0;

QY 164 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCCGCGTTGTTGGGGGA 223
DB 1886 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCCGCGTTGTTGGGGGA 1945

QY 224 GATGATGGGGCGTTAAATTTGSCATGCTAAACAAGATCAGGAAGGGGAAAAGGGC 283
DB 1946 GATGATGGGGCGTTAAATTTGSCATGCTAAACAAGATCAGGAAGGGGAAAAGGGC 2005

QY 284 ACTATGGTTAAATTTTATATATTTCTGCTGCTGCTCAGGCTTAGATGTGCTAGAT 343
DB 2006 ACTATGGTTAAATTTTATATATTTCTGCTGCTGCTCAGGCTTAGATGTGCTAGAT 2065

QY 344 CTTTCCTTCTCTTTTGTGGGAGAAATTTGAATCCCTCAGACTTGTTCATCGGTAGTTT 403
DB 2066 CTTTCCTTCTCTTTTGTGGGAGAAATTTGAATCCCTCAGACTTGTTCATCGGTAGTTT 2125

QY 404 TTCTTTTCATGATTTTGACAAATGACCTCCGCGGAGCTTTTGTGAG 454
DB 2126 TTCTTTTCATGATTTTGACAAATGACCTCCGCGGAGCTTTTGTGAG 2176

RESULT 8
ABT07357
ID ABT07357 standard; DNA; 470 BP.

XX ABT07357;

XX 07-NOV-2002 (first entry)

XX Reporter construct fragment rice actin intron SEQ ID NO: 109.

XX Plant; gene expression control; insect; hormone receptor; fertility;

XX ecdysone receptor; ds.

XX Oryza sativa.

XX WO200261102-A2.

XX 08-AUG-2002.

PF	24-OCT-2001; 2001MO-US051417.
XX	
PR	24-OCT-2000; 2000US-0242969P.
XX	
PA	(SYGN) SYNGENTA PARTICIPATIONS AG.
PI	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX	
DR	WPI; 2002-619259/66.
XX	
PT	New receptor cassette encoding a chimeric receptor polypeptide, useful in
PT	regulating expression of target polypeptides in plants in the presence of
PT	appropriate ligands that may be used in controlling plant fertility.
PS	
XX	Example 10; Page 263; 319pp; English.
CC	The present invention relates to a receptor cassette encoding a chimeric
CC	receptor polypeptide comprising at least one DNA binding domain, a hinge
CC	domain of an ecdysone receptor (ECR) of an insect, a ligand binding
CC	domain of an insect ECR, where the ligand binding domain is heterologous
CC	with respect to the hinge domain and an activation domain. The chimeric
CC	insect hormone receptors and receptor cassettes are useful in regulating
CC	expression of target polypeptides in plants in the presence of
CC	appropriate ligands that may be used in controlling plant fertility. The
CC	method is useful for decreasing or increasing plant gene expression. The
CC	present sequence is a polynucleotide described in the exemplification of
CC	the invention
SQ	
	Sequence 470 BP; 75 A; 103 C; 141 G; 151 T; 0 U; 0 Other;
	Query Match 63.7%; Score 289; DB 6; Length 470;
	Best Local Similarity 100.0%; Pred. No. 1.9e-129;
	Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	166 GGATCCTCGGGGGAATGGGGCTCGCATGTAGATCTGATCGGCCGTTGGGGGAGA 225
DB	166 GGATCCTCGGGGGAATGGGGCTCGCATGTAGATCTATTCGCCGTTGGGGGAGA 225
OY	226 TGATGGGGCGTTAAATTTCGCATGCTTAAACAAGATCAGAGAAGGGAAAAAGGGCAC 285
DB	226 TGATGGGGCGTTAAATTTCGCCATGCTTAAACAAGATCAGAGAAGGGAAAAAGGGCAC 285
OY	286 TAGGTTTAATTTTTTAATATTTTGCTGCTGCTGCTGCTGCAAGCTTAGATGTCATGCT 345
DB	286 TAGGTTTAATTTTTTAATATTTTGCTGCTGCTGCTGCTGCAAGCTTAGATGTCATGCT 345
OY	346 TTCTTCTCTCTTTTGGGGTGAAGTTTGAATCCACACATTTGTCATCGGTAGTTT 405
DB	346 TTCCTTCCTCTTTTGGGGTGAAGTTTGAATCCACACATTTGTCATCGGTAGTTT 405
OY	406 CTTTTCATGATTTTGACAAATGACGCTCGTGGGAGCTTTTGTAG 454
DB	406 CTTTTCATGATTTTGACAAATGACGCTCGTGGGAGCTTTTGTAG 454
	RESULT 9
ID	ADF49181
XX	ADF49181 standard; DNA; 470 BP.
XX	
XX	ADF49181;
DT	12-FEB-2004 (first entry)
DE	Rice actin intron.
XX	
XX	receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW	hinge domain; ecdysone receptor; ECR; ligand binding domain;
KM	activation domain; transgenic seed; transgenic plant; plant line;
KX	herbicide; pesticide; rice; actin; intron; ds.
OS	Oryza sp.
XX	
PN	US2003154509-A1.

XX	PD	14-AUG-2003.
XX	PF	24-OCT-2001; 2001US-00087167.
XX	PR	24-OCT-2001; 2001US-00087167.
XX	PA	(PASC/) PASCAL E. J.
XX	PA	(VALE/) VALENTINE S. A.
XX	PA	(BROW/) BROWN J. A.
XX	PA	(COCK/) COCKRELL A. S.
XX	PA	(JOHN/) JOHNSON B. D.
XX	PI	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX	DR	WPI; 2003-897756/82.
XX	PT	New receptor cassette encoding a chimeric receptor polypeptide, useful
XX	PT	for regulating the expression of target polypeptides in plants in the
XX	PT	presence of appropriate chemical ligands.
XX	PS	Example 10; SEQ ID NO 109; 186pp; English.
XX	CC	The invention describes a receptor cassette encoding a chimeric receptor
XX	CC	polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
XX	CC	(D) domain of an ecdysonic receptor (ECR) of an insect, a ligand binding
XX	CC	(E) domain that is heterologous with respect to the D domain, and an
XX	CC	activation domain. The receptor cassette and method are useful in
XX	CC	regulating the expression of target polypeptides in plants in the
XX	CC	presence of appropriate chemical ligands. The transgenic seeds and plants
XX	CC	can be used for the breeding of improved plant lines that, for e.g.,
XX	CC	increase the effectiveness of conventional methods such as herbicide or
XX	CC	pesticide treatment. This sequence represents a rice actin intron used in
XX	CC	the construction of a monocot-expressible target expression cassette
XX	CC	comprising the firefly luciferase reporter gene and having response
XX	XX	elements for the GML4 DNA binding domain.
XX	SQ	Sequence 470 BP; 75 A; 103 C; 141 G; 151 T; 0 U; 0 Other;
XX	Query Match	63.7%; Score 289; DB 10; Length 470;
XX	Best Local Similarity	100.0%; Pred. No. 1.9e-129;
XX	Matches 289; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	166	GGATCCTCGCGGGAATGCGGCTCTCGGATGTAGATCTGATCCGCCGTTGTTGGGGAGA 225
DB	166	GGATCCTCGCGGGAATGCGGCTCTCGGATGTAGATCTGATCCGCCGTTGTTGGGGAGA 225
QY	226	TGATCGGGCGGTTAAATTTCCGATCGTAAACAAGATCAGGAAGAGGGGAAAAGGGCAGC 285
DB	226	TGATCGGGCGGTTAAATTTCCGATCGTAAACAAGATCAGGAAGAGGGGAAAAGGGCAGC 285
QY	286	TATGGTTAAATTTTAAATATATTTCTGCTGCTGCTGCTCAGGCTTAGATGTAGATCT 345
DB	286	TATGGTTAAATTTTAAATATATTTCTGCTGCTGCTGCTCAGGCTTAGATGTAGATCT 345
QY	346	TTCTTTCTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATGTCTCATTCGCTAGTTT 405
DB	346	TTCTTTCTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATGTCTCATTCGCTAGTTT 405
QY	406	CTTTTCATGATTTTGTGACAATGCAAGCTCTGCGGGAGCTTTTGTGAG 454
DB	406	CTTTTCATGATTTTGTGACAATGCAAGCTCTGCGGGAGCTTTTGTGAG 454
RESULT 10		
ID	ABZ70926	standard; DNA; 1121 BP.
XX	ABZ70926;	
DT	23-APR-2003	(first entry)
XX	CYIIIA 3'	fragment with the 3' end of rice actin 1 intron.

XX Transgenic organism; male sterility; herbicide resistance;
KW insecticide resistance; selectable marker; counter-selectable marker;
KM gene; ds.
XX Oryza sativa.
OS Synthetic.
XX WO200296192-A2.
PN 05-DEC-2002.
PD 05-DEC-2002.
XX 29-APR-2002; 2002WO-EP004724.
PF 29-APR-2002; 2002WO-EP004724.
XX 29-APR-2002; 2002WO-EP004724.
PR 29-APR-2002; 2002WO-EP004724.
XX (ICON-) ICON GENETICS AG.
PA (ICON-) ICON GENETICS AG.
PI Werner S, Marillonnet S, Klimyuk V, Gleba Y;
XX WPI; 2003-041365/03.
DR WPI; 2003-041365/03.
XX Producing a transgenic organism expressing a trait of interest where the
PT trait of interest is involved in male sterility.
XX Example 1; Page 25-26; 42pp; English.
PS The present invention describes a method for producing a transgenic
XX multicellular plant or animal organism expressing a trait of interest and
CC having a controlled distribution of the trait to progeny where the
CC process comprises hybridizing a first multicellular organism or a cell
CC thereof having a first heterologous DNA sequence comprising a first
CC fragment of a nucleotide sequence encoding said trait of interest and a
CC second multicellular organism or a cell thereof having a second
CC heterologous DNA sequence comprising a second fragment of the nucleotide
CC sequence encoding said trait of interest where each first and second
CC heterologous sequences are designed such that the trait of interest
CC arises due to RNA trans-splicing after said hybridisation. The method can
CC be used for producing a transgenic multicellular plant or animal organism
CC expressing a trait of interest where trait of interest is involved in
CC male sterility and is selected form herbicide resistance, insecticide
CC resistance, selectable marker, counter-selectable marker. The present
CC sequence represents a synthetic CryIIIA 3' fragment with the 3' end of
CC rice actin 1 intron, which is used in an example from the present
CC invention
XX
SQ Sequence 1121 BP; 302 A; 284 C; 241 G; 294 T; 0 U; 0 Other;
Query Match 45.8%; Score 208; DB 10; Length 1121;
Best Local Similarity 100.0%; Pred. No. 2.9e-90;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 247 GCCATGCTAAACAAAGATCAGAGAGGGGAAAGGCGACATGCTTATATTTTATATA 306
DB 7 GCCATGCTAAACAAAGATCAGAGAGGGGAAAGGCGACATGCTTATATTTTATATA 66
QY TTTCTGCTGCTGCTGCTCAGGCTAGATGCTAGATCTTCTCTCTTTTGTGGGT 366
DB TTTCTGCTGCTGCTGCTCAGGCTAGATGCTAGATCTTCTCTCTTTTGTGGGT 126
QY 367 AGAATTTGAATCCCTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTGTACAA 426
DB 127 AGAATTTGAATCCCTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTGTACAA 186
QY 427 TGCAGCCTCGTGCAGGAGCTTTTGTAG 454
DB 187 TGCAGCCTCGTGCAGGAGCTTTTGTAG 214

AC ADP73931;
XX 09-SEP-2004 (first entry)
DT Plasmid pDAB8505, SEQ ID NO:85, encoding mAb HX8 (both chains).
XX
DE Transgenic plant; immunoglobulin production; recombinant production;
XX gamma-glycan; fucose; glycan; virucide; immunotherapy; maize;
KW gamma-zein promoter; rice; actin promoter;
KW phosphinothricin acyltransferase; PAT; mouse; leader sequence;
KW herpes simplex virus; HSV1; HSV2; human; monoclonal antibody HX8; IgA;
KW heavy chain; light chain; codon optimised; plasmid; pDAB8505; cyclic;
KM circular; ds.
XX Zea mays.
OS Mus sp.
OS Homo sapiens.
OS Oryza sativa.
OS Chimeric.
OS Synthetic.
OS Unidentified.
XX
FH Key
FH misc_feature
FT Location/Qualifiers
FT 424..1589
FT /tag= a
FT /label= SAR
FT /note= "Scaffold attachment region. Also referred to as
FT MAR (matrix association region)"
FT 1673..3175
FT /tag= b
FT /note= "Maize gamma-zein promoter"
FT 3178..4671
FT /tag= d
FT /product= "Heavy chain of human anti-HSV1/HSV2 monoclonal
FT IgA antibody HX8 (with mouse leader sequence)"
FT 3178..3234
FT /tag= c
FT /note= "Mouse leader sequence"
FT 3235..4668
FT /tag= e
FT /product= "Mature HX8 heavy chain"
FT 4678..5045
FT /tag= f
FT /note= "Maize per5 3'UTR"
FT 5157..6659
FT /tag= g
FT /note= "Maize gamma-zein promoter"
FT 6662..7363
FT /tag= i
FT /product= "Heavy chain of human anti-HSV1/HSV2 monoclonal
FT IgA antibody HX8 (with mouse leader sequence)"
FT 6662..6718
FT /tag= h
FT /note= "Mouse leader sequence"
FT 6719..7360
FT /tag= j
FT /product= "Mature HX8 heavy chain"
FT 7370..7737
FT /tag= k
FT /note= "Maize per5 3'UTR"
FT 7889..9258
FT /tag= l
FT /note= "Rice actin promoter/intron"
FT 9261..9815
FT /tag= m
FT /product= "Phosphinothricin acyltransferase (PAT)"
FT /note= "The PAT coding region is given in the
FT specification as positions 9260-9820"
FT 9831..10162
FT /tag= n
FT /note= "Maize lipase 3'UTR"
FT 10229..11394
FT /tag= o
FT misc_feature

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: September 12, 2005, 05:47:04 ; Search time 1929.56 Seconds
(without alignments)
8956.038 Million cell updates/sec

Title: US-10-758-799-2

Perfect score: 454
Sequence: 1 GTTAAACACACCCGCCCTCTCTC.....CGTGGAGAGCTTTTGTAG 454

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST: *
1: gb_est1.*
2: gb_est2.*
3: gb_hlc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	15.9	542	5	BQ609717 BRY_5803
2	25	5.5	991	9	CL076535 CH216-139
3	24	5.3	1205	9	AG380362 Mus muscu
4	22	4.8	662	7	CU343092 RPL144.27
5	22	4.8	687	9	AG121527 Pan trogl
6	22	4.8	997	6	CB561980 AGENCORT
7	21	4.6	123	9	BM232968 Danio rer
8	21	4.6	430	9	CG198335 PUFMC48TB
9	21	4.6	453	2	BF558554 UI-M-HC-d
10	21	4.6	505	7	CF740605 UI-M-HC-d
11	21	4.6	555	8	AO631272 RPL1-11-4
12	21	4.6	604	8	BH558342 BOG1A74TR
13	21	4.6	654	7	CF828591 UCRCR01_0
14	21	4.6	655	7	CO746318 UCRCR01_0
15	21	4.6	657	7	CF828592 UCRCR01_0
16	21	4.6	743	1	AL693283 AL693283
17	21	4.6	767	1	BY986759 Forward s
18	21	4.6	793	9	AG525416 Mus muscu
19	21	4.6	807	8	B20652 B20652
20	21	4.6	828	9	CG876902 HSC 00941
21	21	4.6	892	5	CL475111 SAIL 231
22	21	4.6	927	5	BK455358 BK455358
23	21	4.6	1071	9	CU103786 ISB1-41P2
24	21	4.6	1077	4	BG105171 602312910

25	21	4.6	1195	9	AG393152 Mus muscu
26	21	4.6	1224	9	AG524895 Mus muscu
27	21	4.6	1345	8	CC238075 CH261-132
28	21	4.6	1712	4	BG760522 602716959
29	20	4.4	139	2	BE138943 xtc63d05.x
30	20	4.4	188	1	AI355517 qc96d12.x
31	20	4.4	214	2	BB524812 BB524812
32	20	4.4	222	2	BB857906 BB857906
33	20	4.4	227	1	AI273903 AI273903
34	20	4.4	235	7	CN38434 CN38434
35	20	4.4	243	4	BM829427 K-EST0102
36	20	4.4	245	8	AZ353546 1M0092A05
37	20	4.4	253	4	B1068455 C022P21U
38	20	4.4	254	4	BF959480 OV2-NN004
39	20	4.4	265	1	AV312223 AV312223
40	20	4.4	268	2	AM948856 QV4-FT000
41	20	4.4	271	4	BG073230 H3120C03-3
42	20	4.4	271	5	BU674968 UI-CF-DU0
43	20	4.4	276	1	AI749380 AI749380
44	20	4.4	277	2	BB301206 BB301206
45	20	4.4	280	2	BB080651 BB080651

ALIGNMENTS

RESULT 1
BQ609717 542 bp mRNA linear EST 25-JUN-2002
LOCUS BRY_5803 wheat EST endosperm library Triticum aestivum cDNA 5',
DEFINITION mRN sequence.
ACCESSION BQ609717 GI:21559056
VERSION BQ609717.1
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 542)
REFERENCE Clarke,B., Lambrecht,M. and Rhee,S.Y.
Arabidopsis genomic information for interpreting wheat EST
sequences
JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 22478026
PUBMED 12590341

COMMENT
Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@comoma.stanford.edu.
location/Qualifiers
1. .542
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultiivar="WYuna"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/clone_lib="wheat EST endosperm library"

FEATURES

source
1. .542
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultiivar="WYuna"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/clone_lib="wheat EST endosperm library"

ORIGIN
Query Match 15.9%: Score 72; DB 5; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.9e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CGCATGCTTAACAGATCAGAAAGGCACTATGTTATATTTTATAT 305
DB 148 CGCATGCTTAACAGATCAGAAAGGCACTATGTTATATTTTATAT 207

```

QY      306 ATTCTGCTGCT 317
      |||||
      208 ATTCTGCTGCT 219

RESULT 2
LOCUS   CL076535
DEFINITION CL076535 991 bp DNA linear GSS 31-DEC-2003
          CH216-139N11.RM1.1 CH216 Xenopus tropicalis genomic clone
          CH216-139N11, genomic survey sequence.
ACCESSION CL076535
VERSION   CL076535
KEYWORDS  GSS.
SOURCE    Xenopus tropicalis (western clawed frog)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
          Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 991)
          Kremetzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
          Wardis,E. and Wilson,R.
          A physical map of the xenopus tropicalis genome
          Unpublished (2003)
          Contact: Richard K Wilson
          Genome Sequencing Center
          Washington University School of Medicine
          Email: submissions@watson.wustl.edu
          Insert Length: 175000 Std Error: 0.00
          Seq primer: RM1 TACGACTCACTATAGCGAGA
          Class: BAC ends
          High quality sequence start: 11
          High quality sequence stop: 99.
FEATURES
  source
    1..991
    /organism="Xenopus tropicalis"
    /mol_type="genomic DNA"
    /strain="Nigerian frog"
    /db_xref="taxon:8364"
    /clone="CH216-139N11"
    /sex="male"
    /cell_line="Stock 248 F7A2, inbred N7"
    /clone_1id="CH216"
    /note="Vector: PTARBAC2.1; CHORI-216 Xenopus tropicalis
    BAC library"

ORIGIN
Query Match 5.5%; Score 25; DB 9; Length 991;
Best Local Similarity 100.0%; Pred.No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCACCCCGCCCTCTCTCTTTCTT 29
      |||||
      680 CCACCCCGCCCTCTCTCTTTCTT 704

RESULT 3
LOCUS   AG380362
DEFINITION AG380362 1205 bp DNA linear GSS 03-JUN-2004
          Mus musculus molossinus DNA, clone:MSWG01-189W20.T7, genomic survey
          sequence.
ACCESSION AG380362
VERSION   AG380362.1 GI:47991567
KEYWORDS  GSS.
SOURCE    Mus musculus molossinus
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
          BAC end Sequences of Library MSWG01
          Unpublished
REFERENCE 2 (bases 1 to 1205)
          Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

```

```

TITLE   Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
1-7-22 Suenho-chou,Tsukuba-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSWG01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY     : pBACe3.6
Vector      : EcoRI
R.Site 1    : EcoRI
R.Site 2    : EcoRI.
FEATURES
  source
    1..1205
    /organism="Mus musculus molossinus"
    /mol_type="genomic DNA"
    /sub_species="molossinus"
    /db_xref="taxon:57486"
    /clone="MSWG01-189W20.T7"
    /sex="male"
    /issue_type="mixture of kidney and spleen"
    /clone_1id="MSWG01 Mouse Male BAC library"

ORIGIN
Query Match 5.3%; Score 24; DB 9; Length 1205;
Best Local Similarity 100.0%; Pred.No. 0.43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CTTTCTTCTCCGTTTTTTTTTTC 46
      |||||
      379 CTTTCTTCTCCGTTTTTTTTTTC 356

RESULT 4
LOCUS   CL343092
DEFINITION CL343092 662 bp DNA linear GSS 19-AUG-2004
          RPCI44.276C24.f RPCI-44 Sus scrofa genomic clone RPCI44_276C24,
          genomic survey sequence.
ACCESSION CL343092
VERSION   CL343092.1 GI:51395060
KEYWORDS  GSS.
SOURCE    Sus scrofa (pig)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
REFERENCE 1 (bases 1 to 662)
          Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Martron,B.M.,
          Beever,J.E. and Schook,L.B.
          Piggy-BACing the Human Genome: Constructing a Porcine Physical Map
          Through Comparative Genomics
          Unpublished (2004)
          Other GSSs: RPCI44_276C24.r
          Contact: Lawrence B. Schook
          Department of Animal Sciences
          University of Illinois at Urbana Champaign
          1201 W. Gregory Dr., Urbana, IL 61801, USA
          Tel: 217 265 5326
          Fax: 217 244 5617
          Email: schook@uiuc.edu
          Clones are derived from the porcine BAC library RPCI-44
          (http://www.bacpac.choi.org/porcine242.htm). For BAC library
          availability, please contact Pieter de Jong (pdjong@choi.org).
          Clones may be purchased from BACPAC Resources
          (http://BACPACorders.choi.org). This work was undertaken as part
          of the International Swine Genome Sequencing Consortium by
          University of Illinois at Urbana Champaign, USA with funds provided

```


by grant No. AG2002-34480-11828 from USDA-CSREES and
AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
Initiative)
Plate: 276 row: C column: 24
Seq primer: T7
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..662
/organism="Sus scrofa"
/mol_type="genomic DNA"
/strain="four pigs (breed: 37.5% Yorks Landrace and 25%
Meishan)"
/db_xref="taxon:9823"
/clone="RPC144_276C24"
/sex="male"
/cell_type="blood"
/clone_id="RPC1-44"
/note="Vector: pFARBAC2; Site 1: ECORI; Site 2: BCGRI;
porcine male BAC library produced by Pieter de Jong"

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 TAGATCTTTCTTTCTTTCTTTT 360
|||||
2 TAGATCTTTCTTTCTTTCTTTT 23

Db

RESULT 5
AG121527 687 bp DNA linear GSS 04-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-130J16.F, genomic survey sequence.
DEFINITION AG121527
ACCESSION AG121527.1 GI:16650692
VERSION
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
AUTHORS

TITLE
JOURNAL
2 (bases 1 to 687)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Aao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chipbes@gsc.riken.go.jp; URL: http://hsp.gsc.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT
Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.

PRIMERS

Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.

FEATURES
source

Location/Qualifiers
1..687
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-130J16.F"
/sex="male"
/cell_type="lymphoblast"
/clone_id="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match 4.8%; Score 22; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCCTCCTCTTTCTTTCTTCC 34
|||||
Db 638 CCCCTCCTCTTTCTTTCTTCC 659

RESULT 6

CB561980 997 bp mRNA linear EST 02-APR-2003
LOCUS AGENCOURT_13324979 NICHHD_XGC_Tad1 Xenopus laevis cDNA clone
DEFINITION IMAGE:6880820 3', mRNA sequence.
CB561980
ACCESSION CB561980.1 GI:29481510
VERSION
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
AUTHORS

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Drs. Donald Brown and Liqun Cai
CDNA Library Preparation: CLONTECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LILNL at:
http://image.llnl.gov
Plate: LILNL3124 row: n column: 19
High quality sequence start: 4
High quality sequence stop: 231.

FEATURES

source

Location/Qualifiers
1..997
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6880820"
/dev_stage="metamorphosis stage 53"
/clone_id="NICHHD_XGC_Tad1"
/note="Organ: Developing Tadpole; Vector: pDNR-LIB;
Site 1: Sfi; Site 2: Sfi; 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTGAGAGCCGAGCGGCCGACGAC-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.6 kb
(range 0.9-3.0 kb). 15/15 colonies contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 4.8%; Score 22; DB 6; Length 997;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CTCCTCTTTCTTTCTTCGTTT 39
|||||
Db 762 CTCCTCTTTCTTTCTTCGTTT 741

RESULT 7

BX232968 123 bp DNA linear GSS 13-MAR-2003
LOCUS BX232968/c
DEFINITION Danio rerio genomic clone DKRY-282L1, genomic survey sequence.

```

ACCESSION   BX232968
VERSION     BX232968.1  GI:28067118
KEYWORDS
SOURCE      Dario rerio (zebrafish)
ORGANISM    Dario rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 123)
AUTHORS     Humphray, S.J., Huckle, E. and Durham, J.L.
TITLE       Direct Submision
JOURNAL     Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humphray@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 282L1. 282L1 is
            part of the Dariokey BAC library created by R. Plaeterk and N.V.
            Keygene. Further details:
            http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES
    source
        1..123
            /organism="Dario rerio"
            /mol_type="genomic DNA"
            /db_xref="taxon:7955"
            /clone="DKEY-282L1"
            /issue_type="Testis"
            /note="Vector pindigobAC-536"

ORIGIN
Query Match      4.6%; Score 21; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      292 TTATATTTTATATATTTCTG 312
       75 TTATATTTTATATATTTCTG 55

RESULT 8
LOCUS     CG198335      430 bp      DNA      linear      GSS 21-AUG-2003
DEFINITION
            pUPMC487B_ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTA0681H23,
            genomic survey sequence.
ACCESSION   CG198335
VERSION     CG198335.1  GI:34089396
KEYWORDS    GSS.
SOURCE      Zea mays
            Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 430)
AUTHORS     Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
            Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
            Bennettzen, J.
TITLE       Maize Genomics Consortium
JOURNAL     Unpublished (2003)
COMMENT     Other_GSSs: pUPMC487D
            Contact: Cathy Whiteley
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whiteley@tigr.org
            Seq primer: TR
            Class: sheared ends.
            Location/Qualifiers
                1..430
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /strain="B73"
                    /db_xref="taxon:4577"
                    /clone="ZMMBTA0681H23"
                    /clone_1tb="ZM_0.6_1.0_KB"

```

```

/Note="Vector: pCRA-TOPO, Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN
Query Match      4.6%; Score 21; DB 9; Length 430;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      343 TCTTCTTCTCTCTTTTGTG 363
       172 TCTTCTTCTCTCTTTTGTG 152

RESULT 9
LOCUS     BF558554/c      453 bp      mRNA      linear      EST 12-DEC-2000
DEFINITION   BF558554
            UI-R-E0-dg-f-11-0-UI.r1 UI-R-E0 Rattus norvegicus cDNA clone
            BF558554
            UI-R-E0-dg-f-11-0-UI 5', mRNA sequence.
ACCESSION   BF558554.1  GI:11668284
VERSION     BF558554
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
            Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 453)
AUTHORS     Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE       Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
MEDLINE     97044477
PUBMED      8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@iowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LNLB (info@image.llnl.gov). IMAGE ID=177947 The following
            repetitive elements were found in this cDNA sequence: 14-73,
            >POLY_A#Simple_repeat 91-239, >B1_MM#SINE/Alu 293-414,
            >(GAAA)n#Simple_repeat
            Seq primer: M13 Forward.
            Location/Qualifiers
                1..453
                    /organism="Rattus norvegicus"
                    /mol_type="mRNA"
                    /strain="Sprague-Dawley"
                    /db_xref="taxon:10116"
                    /clone="UI-R-E0-dg-f-11-0-UI"
                    /dev_stage="embryonic"
                    /lab_host="DH10B (Life Technologies)"
                    /clone_1tb="UI-R-E0"
                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                    polylinker; Site_1: NotI; Site_2: EcoRI; This library
                    consists of a mixture of individually tagged normalized
                    libraries constructed from 8, 12 and 18-day embryo. The
                    tag is a string of 3-5 nucleotides present between the
                    Not I site and the oligo-dT track which allows
                    identification of the library of origin of a clone within
                    the mixture."

```

```

ORIGIN
Query Match      4.6%; Score 21; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      343 TCTTCTTCTCTCTTTTGTG 363

```

Db 302 TCTTTCTTCTCTTTGTC 282

RESULT 10
CF740605/c
LOCUS
DEFINITION
CF740605
505 bp mRNA linear EST 10-OCT-2003
UI-M-HCO-cky-j-06-0-UI.r1 NIH-BMAP_HCO Mus musculus cDNA clone
IMAGE:30609533 5', mRNA sequence.
ACCESSION
CF740605
VERSION
CF740605.1 GI:37636943
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James Ian University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
National Institutes of Health, Mammalian Gene Collection (MGC)

The following repetitive elements were found in this cDNA
sequence: 375-414, >(CAAA)n#simple_repeat (matched complement)
Seq primer: pYX-5.

FEATURES
source
Location/Qualifiers

1..505
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30609533"
/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1lb="NIH_BMAP_HCO"
/note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTAATGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

ORIGIN

Query Match 4.6%; Score 21; DB 7; Length 505;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 AGATCTTCTTCTTCTTTT 360
|||||
Db 38 AGATCTTCTTCTTCTTTT 18

RESULT 11
A0631272/c
LOCUS
DEFINITION
R0CT-11-482H7.TV R0CT-11 Homo sapiens genomic clone R0CT-11-482H7,
555 bp DNA linear GSS 17-JUN-1999

genomic survey sequence.

ACCESSION
A0631272
VERSION
A0631272.1 GI:5093907
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Shanying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeet@igf.org
Clones are derived from the human BAC library R0CT-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.bufileo.edu/ordering>) or from
Research Genet cs (http://www.tigr.org/cdb/hungen/bac_end_search.html).
Seq primer: T7
Class: BAC ends.

FEATURES
source
Location/Qualifiers

1..555
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7684878"
/db_xref="taxon:9606"
/clone="R0CT-11-482H7"
/sex="Male"
/cell_type="Lymphocytes"
/clone_1lb="R0CT-11"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
RC111 Human Male BAC Library"

ORIGIN
Query Match 4.6%; Score 21; DB 8; Length 555;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 AGATCTTCTTCTTCTTTT 360
|||||
Db 333 AGATCTTCTTCTTCTTTT 313

RESULT 12
BH558342/c
LOCUS
DEFINITION
BOGIA74TR BOGI Brassica oleracea genomic clone BOGIA74, genomic
survey sequence.
ACCESSION
BH558342
VERSION
BH558342.1 GI:117810122
KEYWORDS
GSS.
SOURCE
Brassica oleracea
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOGIA74TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtowne@igf.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.

FEATURES

source
 1. 604
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone_1ib="BOGIA74"
 /note="Vector: pHOSt; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOSt using BstXI linkers"

ORIGIN

Query Match 4.6%; Score 21; DB 8; Length 604;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 291 TTTATATTTTATATATTTCT 311
 |||||
 Db 305 TTTATATTTTATATATTTCT 285

RESULT 13
 CF828591 654 bp mRNA linear EST 29-OCT-2003
 LOCUS UCRCH01.01N03 f Clementine Mandarin Albedo at Rind Separation cDNA
 DEFINITION Library Citrus reticulata cDNA clone CR_CEA01N03, mRNA sequence.
 ACCESSION CF828591
 VERSION CF828591.1 GI:38026291
 KEYWORDS EST.
 SOURCE Citrus reticulata
 ORGANISM Citrus reticulata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Sapindales; Rutaceae; Citrus.
 1 (bases 1 to 654)
 Close,T.J., Roose,M.L., Federici,C.F., Mu,L., Fenton,R.D.,
 Manamaker,S., Kahn,T., Williams,T., Lovatt,C., Kim,H.R., Kudrna,D.,
 Wing,R. and Yu,Y.
 Development of EST Resources and New Genetic Markers for California
 Citrus Clementine Mandarin Albedo at Rind Separation
 Unpublished (2003)
 Contact: Timothy Close
 Department of Botany & Plant Sciences, University of California
 Riverside, CA, 92521-0124
 Tel: 9097873318
 Fax: 9097874437
 Email: timothy.close@ucr.edu
 Seq primer: T7.

FEATURES

source
 1. 654
 /organism="Citrus reticulata"
 /mol_type="mRNA"
 /cultivar="Clementina Fina Sodea"
 /db_xref="taxon:85571"
 /clone="CR_CEA01N03"
 /tissue_type="Albedo"
 /dev_stage="12 year old trees"
 /lab_host="E. coli TUC121"
 /clone_1ib="Clementine Mandarin Albedo at Rind Separation cDNA Library"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI; Site 2: XhoI; Rind separation is a
 prominent trait in Clementines. Kahn and Williams (UC
 Riverside) advised that the best Clementine for this trait
 is Fina Sodea. Lovatt (UC Riverside) provided advice on
 which portion of the peel would be most likely to contain
 transcripts related to rind separation. Federici (Roose

ORIGIN

Query Match 4.6%; Score 21; DB 7; Length 654;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 350 TTCTCTTTTGTGGTAGAA 370
 |||||
 Db 562 TTCTCTTTTGTGGTAGAA 582

RESULT 14
 CO746318 655 bp mRNA linear EST 30-JUL-2004
 LOCUS CO746318/c ta869a09.y1 Hydra EST UCI 5 Hydra magnipapillata cDNA 5' similar to
 DEFINITION SW:CLH1_HUMAN Q00610 CLATHRIN HEAVY CHAIN 1;; mRNA sequence.
 ACCESSION CO746318
 VERSION CO746318.1 GI:50861127
 KEYWORDS EST.
 SOURCE Hydra magnipapillata
 ORGANISM Hydra magnipapillata
 Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
 Hydridae; Hydra.
 1 (bases 1 to 655)
 Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
 Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marx,M.,
 Hillier,L., Martin,J., Wylie,T., Dame,M., Theising,B., Bowers,Y.,
 Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R.,
 Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
 WashU Hydra EST Project
 Unpublished (2002)
 Contact: Hans Bode
 WashU Hydra EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Library was constructed by Dirk Lindgens, Univ. of Calif. Irvine
 library materials provided by Hans Bode & Dirk Lindgens, Univ. of
 Calif., Irvine DNA sequencing by: Washington University Genome
 Sequencing Center For information on obtaining a clone please
 contact: Hans Bode (hnbode@uci.edu)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 470.

FEATURES

source
 1. 655
 /organism="Hydra magnipapillata"

```

/mol_type="mRNA"
/strain="105"
/db_xref="taxon:6085"
/lab_host="DH10B"
/clone_id="Hydra EST UCI 5"
/notes="Vector: pSPORT1; Site 1: Not I; Site 2: Sal I;
a.1 strand cDNA was primed with a Not I primer-adaptor
(5' - pGACTAGTCTAGATCGGACGGCCGCTT)15-3')
b. Double-stranded cDNA was ligated to Sal I adaptor,
digested with Not I and cloned into the pSPORT 1-vector
pre-cut with Not I and Sal I. c. The ligation mix was
transformed into DH10B cells. d. The cells were grown in
SOC = 5g yeast, 20g tryptone, 0.5g NaCl, 10 mM MgSO4, 10
mM MgCl, 0.2% glucose/liter, (no antibiotic). e. DMSO was
added to a final conc. of 10% as a cryoprotectant and
frozen f. The litre before freezing was determined as
~2400/100 ul. Assuming a 10% loss upon freezing, the litre
is probably ~2100/100 ul. g. 9 tubes each containing ~
2100 clones/100 ul (= total of ~19,000) are enclosed.
h. The frequency of vectors containing inserts is 96% as
determined by digestion check after picking 24 clones,
mini-prep and subsequent digestion with Not I and Sal I.
i. A low level of 32p was used in the cDNA synthesis
procedure. The level measured by holding a Geiger Counter
next to a tube was background."

```

ORIGIN

Query Match

```

Best Local Similarity 100.0%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 293 TATATTTTATATATTTCTGC 313
    |||||||||||||||||||
Db 549 TATATTTTATATATTTCTGC 529

```

```

4.6%; Score 21; DB 7; Length 655;

```

ORIGIN

Query Match

```

Best Local Similarity 100.0%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 350 TTCTTCTTTTGTGGGTAGAA 370
    |||||||||||||||||||
Db 93 TTCTTCTTTTGTGGGTAGAA 73

```

```

Search completed: September 12, 2005, 14:04:06
Job time : 1937.56 secs

```

/clone_11b="Clementine Mandarin Albado at Rind Separation cDNA Library"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: ScaRI; Site 2: XhoI; Rind separation is a prominent trait in Clementines. Kahn and Williams (UC Riverside) advised that the best Clementine for this trait is Fina Sodea. Lovatt (UC Riverside) provided advice on which portion of the peel would be most likely to contain transcripts related to rind separation. Federici (Roose lab) collected twenty fruit in November 2002 and with assistance from Mu (Roose lab) pulled off pieces of peel, and then cut the inner 2 mm of albedo that was adjacent to the fruit and snap froze this material in liquid nitrogen. The fruit were beginning to turn orange but were still mostly green and were moderately easy to peel, with some easier than others. Frozen tissues were stored at -80C until further processing. Fenton (Close lab) purified RNA by the phenol method described in T. Japanese Soc. Hort. Sci. 1996. 64 (4) : 809-814, purified poly(A) mRNA using a PolyAtrick mRNA isolation System IV (Promega), produced a primary cDNA library using a Lambda ZAP XR cDNA Synthesis Kit (Stratagene), then mass-excised one million pfu from the primary library to produce a phagemid population. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute, University of Arizona (Kim, Kudrna, Wing, Yu). Chromatogram files were downloaded by FTP to UC Riverside (by Close), then processed at UC Riverside (by Manamaker, Close lab) using the HarvEST pipeline (<http://harvest.ucr.edu>) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a primed 17 region of at least 100 bases were deposited to GenBank."

```

RESULT 15
CF828592/c
LOCUS
DEFINITION
UCRRCR01.01N03_r Clementine Mandarin Albado at Rind Separation cDNA
Library Citrus reticulata cDNA clone CR_CEA01N03, mRNA sequence.
ACCESSION
CF828592
VERSION
CF828592.1 GI:38026293
KEYWORDS
EST.
SOURCE
Citrus reticulata
ORGANISM
Citrus reticulata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Sapindales; Rutaceae; Citrus.
1 (bases 1 to 657)
Close,T.J., Roose,M.L., Federici,C.F., Mu,L., Fenton,R.D.,
Manamaker,S., Kahn,T., Williams,T., Lovatt,C., Kim,H.R., Kudrna,D.,
Wing,R. and Yu,Y.
Development of EST Resources and New Genetic Markers for California
Citrus - Clementine Mandarin Albado at Rind Separation
Unpublished (2003)
Contact: Timothy Close
Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124
Tel: 9097873318
Fax: 9097874437
Email: timothy.close@ucr.edu
Seq primer: T3.
Location/Qualifiers
1..657
/organism="Citrus reticulata"
/mol_type="mRNA"
/cultivar="Clementina Fina Sodea"
/db_xref="taxon:85571"
/clone="CR_CEA01N03"
/tissue_type="Albedo"
/dev_stage="12 year old trees"
/lab_host="B. coli TUC121"
FEATURES
source

```


OY	61	CTTTGGCCCTGGTAGTTTGGGTGGGGGAGAAAGCGGCTTCGTCCGCCAGATCGAGCGCGGG	120
Db	61	CTTTGGCCCTGGTAGTTTGGGTGGGGGAGAAAGCGGCTTCGTCCGCCAGATCGAGCGCGGG	120
OY	121	AGGGCGGGATCTCGCGGCTGGCGGTCTCCGGGGGTAGTCGAGCCCGGATCCTCGCGGGGA	180
Db	121	AGGGCGGGATCTCGCGGCTGGCGGTCTCCGGGGGTAGTCGAGCCCGGATCCTCGCGGGGA	180
OY	181	ATGGGGCTCTCGGATGTAGATCTGAATCCGCGGTGTGGGGGAGATGATGGGGCGTTTAA	240
Db	181	ATGGGGCTCTCGGATGTAGATCTGAATCCGCGGTGTGGGGGAGATGATGGGGCGTTTAA	240
OY	241	AATTTGCGCATCTAAACAAGATCAGAGAGGGGGAAAAGGACATATGGTTATATTTT	300
Db	241	AATTTGCGCATCTAAACAAGATCAGAGAGGGGGAAAAGGACATATGGTTATATTTT	300
OY	301	TATATATTTCTGCTGCTCGTCAAGGCTTAGATGTGCTAGATCTTCTCTTCTTCTT	360
Db	301	TATATATTTCTGCTGCTCGTCAAGGCTTAGATGTGCTAGATCTTCTCTTCTTCTT	360
OY	361	GTGGGTAGATTTGAATCCCTCAGCAATGTTCATCGGTAGTTTCTTTTCAATGATTTGT	420
Db	361	GTGGGTAGATTTGAATCCCTCAGCAATGTTCATCGGTAGTTTCTTTTCAATGATTTGT	420
OY	421	GACCAATGCAGCGCTGGGGAGCTTTTTTTTGTAG	454
Db	421	GACCAATGCAGCGCTGGGGAGCTTTTTTTTGTAG	454

RESULT 2
US-09-037-531-3
; Sequence 3, Application US/09037531

```

1 GENERAL INFORMATION:
2
3 APPLICANT: DeRose, Richard
4
5 APPLICANT: Freysinet, Georges
6
7 TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
8
9 TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
10
11 TITLE OF INVENTION: And Transformed Plant
12
13 NUMBER OF SEQUENCES: 5
14
15 CORRESPONDENCE ADDRESS:
16
17 ADDRESSER: Connolly, Bove, Lodge, & Hutz
18
19 STREET: 1220 Market Street
20
21 CITY: Wilmington
22
23 STATE: DE
24
25 COUNTRY: USA
26
27 ZIP: 19899
28
29 COMPUTER READABLE FORM:
30
31 MEDIUM TYPE: Floppy disk
32
33 COMPUTER: IBM PC compatible
34
35 OPERATING SYSTEM: PC-DOS/MS-DOS
36
37 SOFTWARE: Patent In Release #1.0, Version #1.25
38
39 CURRENT APPLICATION DATA:
40
41 APPLICATION NUMBER: US/09/037,531
42
43 FILING DATE: 10-MAR-1998
44
45 CLASSIFICATION: 800
46
47 ATTORNEY/AGENT INFORMATION:
48
49 NAME: McMorrow Jr., Robert G.
50
51 REGISTRATION NUMBER: 30962
52
53 REFERENCE/DOCKET NUMBER: 5500*24
54
55 TELECOMMUNICATION INFORMATION:
56
57 TELEPHONE: (302)658-9141
58
59 INFORMATION FOR SEQ ID NO: 3:
60
61 SEQUENCE CHARACTERISTICS:
62
63 LENGTH: 1565 base pairs
64
65 TYPE: nucleic acid
66
67 STRANDEDNESS: single
68
69 TOPOLOGY: linear
70
71 MOLECULE TYPE: DNA (genomic)
72
73 US-09-037-531-3

```

Matches	454	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Qy	1	GTAAACACCCCGCCCTCTCCCTCTTTCTTTCTCCGTTTTTTTTTTCGCTCGGCTCGAT							60
Db	1102	GTAAACACCCCGCCCTCTCTCTTTCTTTCTCCGTTTTTTTTTTCGCTCGGCTCGAT							1164
Qy	61	CTTTAGCCTTGTAAGTTGGGTGGGCGAGACGCGCTTCGTCGCCAGATCGGTGGCGGG							120
Db	1162	CTTTAGCCTTGTAAGTTGGGTGGGCGAGACGCGCTTCGTCGCCAGATCGGTGGCGGG							1222
Qy	121	AGGGGCGGGAATCTCGCGGCTGGGCTCTTCGGGGCTGAATCGGCCCCGATCTCTCGGGGGA							180
Db	1222	AGGGGCGGGAATCTCGCGGCTGGGCTCTTCGGGGCTGAATCGGCCCCGATCTCTCGGGGGA							1281
Qy	181	ATGGGGCTCTCGAATGATATCTGATCGCGCGTTGTTGGGGGAATGATGGGGCGTTTAA							240
Db	1282	ATGGGGCTCTCGAATGATATCTGATCGCGCGTTGTTGGGGGAATGATGGGGCGTTTAA							1341
Qy	241	AATTTCCGATGCTPAAACAGATCAGGAAAGGGGAAAGGGCACTATGTTTATATTTT							300
Db	1342	AATTTCCGATGCTPAAACAGATCAGGAAAGGGGAAAGGGCACTATGTTTATATTTT							1401
Qy	301	TATATATTTTCGCTGCTGCTGTCAGGGTTGATGTGTAGATCTTTCTTTCTTTCTTTT							360
Db	1402	TATATATTTTCGCTGCTGCTGTCAGGGTTGATGTGTAGATCTTTCTTTCTTTCTTTT							1461
Qy	361	GTGGGTGAATTTGAATTCCTCAGCATTTTCATCGTAGTTTTTCTTTTCATGATTTGT							420
Db	1462	GTGGGTGAATTTGAATTCCTCAGCATTTTCATCGTAGTTTTTCTTTTCATGATTTGT							1521
Qy	421	GACAAATGCAGCCTCGTGGGAGTTTCTTTTGTAG							454
Db	1522	GACAAATGCAGCCTCGTGGGAGTTTCTTTTGTAG							1555

RESULT 3
US-09-078-862-5
; Sequence 5, Application US/09078862

GENERAL INFORMATION:
APPLICANT: Nan, Guo-Jing
APPLICANT: Nagai, Chitumi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC
TITLE OF INVENTION: TRANSFORMATION OF PINEAPPLE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,862
FILING DATE: 14-MAY-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UH-03321
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 623 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

Query Match	100.0%;	Score 454;	DB 4;	Length 1565;
Best Local Similarity	100.0%;	Pred. NO. 4.3e-211;		

```
;
;
;
TYPE: nucleic acid
STRANDEDNESS: double
```



```

;          TOPOLOGY: circular
;          MOLECULE TYPE: other nucleic acid
;          DESCRIPTION: /desc = "DNA"
US-09-078-862-5

```

Query Match 64.1%; Score 291; DB 3; Length 623;
Best Local Similarity 100.0%; Pred. NC. 8.8e-132;
Matches 291; Conservative 0; Mismatches 0; Gaps 0;

Qy	224	GATGATGGGGCGTTTAAAAATTTGGCATGCTAAACAGATCGAGAAAGGGGAAAAGGCG	283
Db	338	GATGATGGGGCGTTTAAAAATTTGGCATCTAAACAGATCAGAAAGGGGAAAAGGCG	397
Qy	284	ACATAGGTTAATTTTAAATATTTTCGCTGCTGCTGTCAGGCTTAGATGTCGTAGAT	344
Db	398	ACATAGGTTAATTTTAAATATTTTCGCTGCTGCTGTCAGGCTTAGATGTCGTAGAT	457
Qy	344	CTTCTCTTCTCTTTTGGGGAGAAATGGAATCCCTCAGCAATGTTTCATCGGAGATT	403
Db	458	CTTCTCTTCTCTTTTGGGGAGAAATGGAATCCCTCAGCAATGTTTCATCGGAGATT	511

```

Oy      404  TTTCTTTCATGATTTTGTCACAAATGACGCTCGTGGGAGCTTTTGTAG 454
         |||||
Db      518  TTTCTTTCATGATTTTGTCACAAATGACGCTCGTGGGAGCTTTTGTAG 568

```

```

RESULT 4
US-08-144-602B-6
; Sequence 6, Application US/08144602B
; Patent No. 5641876
; GENERAL INFORMATION:
; APPLICANT: MCELROY, David
; APPLICANT: Wu, Ray
; TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: CLINTON SQUARE, P.O. BOX 1051
; CITY: ROCHESTER
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,602B
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TIMIAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/10140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
;
US-08-144-602B-6
Query Match 64.1%; Score 291; DB 1; Length 1392
Beet Local Similarity 100.0%; Pred. No. 8.8e-132;

```

[illegible]

```

RESULT 5
US-08-144-602B-7
; Sequence 7, Application US/08144602B
; Patent No. 5641876
; GENERAL INFORMATION:
; APPLICANT: McElroy, David
; APPLICANT: Wu, Ray
; TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: CLINTON SQUARE, P.O. BOX 1051
; CITY: ROCHESTER
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,602B
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TIMIAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/10140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-144-602B-7

Query Match 64.1%; Score 291; DB 1; Length 1404;
Best Local Similarity 100.0%; Freq. No. 8.8e-132;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 164 CCGGATCTCGCGGGGATGGGCTCCGGATGTAGATCGCGCTGTGTGGGGGA 223
|||
Db 1086 CCGAGTCTCGCGGGGATGGGCTCTCGAGTGAATCTGATCCGCGTGTGGGGGA 1145
|||

224 GATGATGGGCGTTTAAATTTGGCCATGCTAAACAAGATCAGGAAGAGGGAAAAAGGC 283

```

Dd	1146	GATGATGGGGCTTTAAATTTCCGCACTGCTAAACAATCAGGAGAGGGGAAAGGCG	1205
Qy	284	ACTATGGTTTATTTTATATATTTCTGCTGCTGCTGACGCTTGATGTGTAGAT	343
Dd	1206	ACTATGGTTTATTTTATATATTTCTGCTGCTGCTGACGCTTGATGTGTAGAT	1265
Qy	344	CTTCTTTCTTTCTTTTGTGGTAGAATTTGATCCCTCAGCATTTTCATCGTAGTTT	403
Dd	1266	CTTCTTTCTTTCTTTTGTGGTAGAATTTGATCCCTCAGCATTTTCATCGTAGTTT	1325
Qy	404	TTCTTTTCATGATTTGTGACAAATGCAGCCTGTGCGGAGCTTTTGTAG	454
Dd	1326	TTCTTTTCATGATTTGTGACAAATGCAGCCTGTGCGGAGCTTTTGTAG	1376

RESULT 6
US-08-144-602B-5
: Sequence 5, Application US/08144602B

1 APPLICANT: McElroy, David
2 APPLICANT: Wu, Ray
3 TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
4 NUMBER OF SEQUENCES: 27
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
7 STREET: CLINTON SQUARE, P.O. BOX 1051
8 CITY: ROCHESTER
9 STATE: NEW YORK
10 COUNTRY: USA
11 ZIP: 14603
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/144,602B
20 FILING DATE: 27-OCT-1993
21 CLASSIFICATION: 536
22 ATTORNEY/AGENT INFORMATION:
23 NAME: TIMIAN, SUSAN J.
24 REGISTRATION NUMBER: 34,103
25 REFERENCE/DOCKET NUMBER: 19603/10140
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 716-263-1636
28 TELEFAX: 716-263-1600
29 INFORMATION FOR SEQ ID NO: 5:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 2199 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 MOLECULE TYPE: cDNA
36 US-08-144-602B-5

Query Match	64.1%	Score 291	DB 1	Length 2199
Best Local Similarity	100.0%	Pred. NO.	8.9e-132	
Matches 291	0	Mismatches	0	Gaps 0

QY	184	QY	1883	QY	224	Db	1943	QY	284	Db	2003
	CCGAGATCCTCGCGGGGAAATGGGGGCTCTCGAGATGTAGATCTGATCCGCGGTTGTGGGGGA		CCGAGATCCTCGCGGGGAAATGGGGGCTCTCGAGATGTAGATCTGATCCGCGGTTGTGGGGGA		GATGATGGGGGCGCTTTAAAAATTTGGCGATGCTTAAACAAGATCAGGAAAGGGGAAAAAGGGC		GATGATGGGGGCGCTTTAAAAATTTGGCGATGCTTAAACAAGATCAGGAAAGGGGAAAAAGGGC		ACTATGCTTTATATATTTTATATATATTTCTGCTGCTGCTGCTCAGGCTTATGATGTGCTAGAT		ACTATGCTTTATATATTTTATATATATTTCTGCTGCTGCTGCTGCTCAGGCTTATGATGTGCTAGAT
	223		1947		283		2007		343		2062

Accession	Sequence	Length
OY	CTTCTTTCCTCTTTTGTGGGTGAATTTGAATCCCTCAGCATGTTCATCGTAGTTT	403
Db	CTTCTTTCCTCTTTTGTGGGTGAATTTGAATCCCTCAGCATGTTCATCGTAGTTT	2063
OY	TTCTTTTCATATTGTGACAAATGACGACCTCGTGGGAGCTTTTTTTTAA	454
Db	TTCTTTTCATATTGTGACAAATGACGACCTCGTGGGAGCTTTTTTTTAA	2123

RESULT 7
US-08-144-602B-4
; Sequence 4, Application US/08144602B

1 APPLICANT: McELROY, David
 2 APPLICANT: Wu, Ray
 3 TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
 4 NUMBER OF SEQUENCES: 27
 5 CORRESPONDENCE ADDRESS:
 6 ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
 7 STREET: CLINTON SQUARE, P.O. BOX 1051
 8 CITY: ROCHESTER
 9 STATE: NEW YORK
 10 COUNTRY: USA
 11 ZIP: 14603
 12
 13 COMPUTER READABLE FORM:
 14 MEDIUM TYPE: floppy disk
 15 COMPUTER: IBM PC compatible
 16 OPERATING SYSTEM: PC-DOS/MS-DOS
 17 SOFTWARE: Patem in Release #1.0, Version #1.30
 18 CURRENT APPLICATION DATA:
 19 APPLICATION NUMBER: US/08/144,602B
 20 FILING DATE: 27-OCT-1993
 21 CLASSIFICATION: 536
 22 ATTORNEY/AGENT INFORMATION:
 23 NAME: TIMIAN, SUSAN J.
 24 REGISTRATION NUMBER: 34,103
 25 REFERENCE/DOCKET NUMBER: 19603/10140
 26 TELECOMMUNICATION INFORMATION:
 27 TELEPHONE: 716-263-1636
 28 TELEFAX: 716-263-1600
 29 INFORMATION FOR SEQ ID NO: 4:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 5643 base pairs
 32 TYPE: nucleic acid
 33 STRANDEDNESS: single
 34 TOPOLOGY: linear
 35
 36 MOLECULE TYPE: CDNA
 37
 38 US-08-144-602B-4

Query Match 64.1%; Score 291; DB 1; Length 5643;
 Best Local Similarity 100.0%; Pred. No. 8,9e-133;
 Matches 291; Conservative 0; Mismatches 0; Gaps 0

QY	164	CCGATCTCTCCCGGGGAAATGGGAGCTCTCCGATGTAGATCTCATCCGCGTGTGTGGGAGG	223
Db	1886	CCGATCTCTCCCGGGGAAATGGGAGCTCTCCGATGTAGATCTCATCCGCGTGTGTGGGAGG	1945
QY	224	GATGATGGGGCGTTTAAATTTCCGCATGCTAAACAAGATTAGAGAAAGGGGAAAAGGCG	283
Db	1946	GATGATGGGGCGTTTAAATTTCCGCATGCTAAACAAGATTAGAGAAAGGGGAAAAGGCG	2005
QY	284	ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGTCAGGCTTAGATGTCTAGAT	343
Db	2006	ACTATGGTTATATTTTATATATTTCTGCTGCTGCTGTCAGGCTTAGATGTCTAGAT	2065
QY	344	CTTTCCTTCTCTTTTGTGGGAGAAATTGAATCCCTCAGCATGTGTTCATCGTAGTTT	403
Db	2066	CTTTCCTTCTCTTTTGTGGGAGAAATTGAATCCCTCAGCATGTGTTCATCGTAGTTT	2125
QY	404	TTCTTTTATGATTTTGACAACAATGCAGCCCTGTCGGAGAGTTTTTTGTAG	454
Db	2126	TTCTTTTATGATTTTGACAACAATGCAGCCCTGTCGGAGAGTTTTTTGTAG	2176

```
RESULT 8
US-09-377-466B-19
; Sequence 19, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: promoter
; LOCATION: (14)..(235)
; OTHER INFORMATION: cassette
; NAME/KEY: 5'UTR
; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Os.Act1
; NAME/KEY: CDS
; LOCATION: (811)..(2769)
; OTHER INFORMATION: Cry3Bb1 variant 11231mv1
; NAME/KEY: terminator
; LOCATION: (2787)..(3020)
; OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-19

Query Match          29.7%; Score 135; DB 4; Length 3039;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      320 TCGTCAGGCTTAGATGCTAGATCTTCTTCTTTTGTGGTAGAATTGAAATCC 379
        |||||||
DB      660 TCGTCAGGCTTAGATGCTAGATCTTCTTCTTTGTGGTAGAATTGAAATCC 719

QY      380 CTCGACATTTGATCGGTAGTTTCTTTTCATGATTGACAATGACGCTCGTGC 439
        |||||||
DB      720 CTCGACATTTGATCGGTAGTTTCTTTTCATGATTGACAATGACGCTCGTGC 779

QY      440 GGAGCTTTTGTAG 454
        |||||||
DB      780 GGAGCTTTTGTAG 794

RESULT 9
US-09-377-466B-21
; Sequence 21, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
```

```
OTHER INFORMATION: cassette
; NAME/KEY: promoter
; LOCATION: (14)..(235)
; OTHER INFORMATION: P-CaMV.AS4
; NAME/KEY: 5'UTR
; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Os.Act1
; NAME/KEY: CDS
; LOCATION: (811)..(2769)
; OTHER INFORMATION: Cry3Bb1 variant 11231mv2
; NAME/KEY: terminator
; LOCATION: (2787)..(3020)
; OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-21

Query Match          29.7%; Score 135; DB 4; Length 3039;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      320 TCGTCAGGCTTAGATGCTAGATCTTCTTCTTTTGTGGTAGAATTGAAATCC 379
        |||||||
DB      660 TCGTCAGGCTTAGATGCTAGATCTTCTTCTTTGTGGTAGAATTGAAATCC 719

QY      380 CTCGACATTTGATCGGTAGTTTCTTTTCATGATTGACAATGACGCTCGTGC 439
        |||||||
DB      720 CTCGACATTTGATCGGTAGTTTCTTTTCATGATTGACAATGACGCTCGTGC 779

QY      440 GGAGCTTTTGTAG 454
        |||||||
DB      780 GGAGCTTTTGTAG 794

RESULT 10
US-09-377-466B-38
; Sequence 38, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 3044
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: promoter
; LOCATION: (14)..(235)
; OTHER INFORMATION: P-CaMV.AS4
; NAME/KEY: 5'UTR
; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Os.Act1
; NAME/KEY: CDS
; LOCATION: (811)..(2769)
; OTHER INFORMATION: variant Cry3Bb1 coding sequence encoding v11231
; NAME/KEY: terminator
; LOCATION: (2792)..(3025)
; OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-38

Query Match          29.7%; Score 135; DB 4; Length 3044;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
```

```
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 320 TCCTCAGGCTTAGATGTCAGATCTTCTTCTTCTTTGGGAGAAATTGAATCC 379
DB 660 TCCTCAGGCTTAGATGTCAGATCTTCTTCTTCTTTGGGAGAAATTGAATCC 719
QY 380 CTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTTGACAATGAGCCTCGTGC 439
DB 720 CTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTTGACAATGAGCCTCGTGC 779
QY 440 GGAGCTTTTGTAG 454
DB 780 GGAGCTTTTGTAG 794

RESULT 11
US-09-377-466B-17
; Sequence 17, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 3450
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: promoter
; LOCATION: (14)..(235)
; OTHER INFORMATION: P-CaMV.AS4
; NAME/KEY: 5'UTR
; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: Intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Os.Act1
; NAME/KEY: transit peptide
; LOCATION: (825)..(971)
; OTHER INFORMATION: amino terminal TS-Zm.rbcs
; NAME/KEY: Intron
; LOCATION: (972)..(1134)
; OTHER INFORMATION: I-Zm.rbcs
; NAME/KEY: transit peptide
; LOCATION: (1135)..(1221)
; OTHER INFORMATION: carboxy terminus TS-Zm.rbcs
; NAME/KEY: CDS
; LOCATION: (1222)..(3180)
; OTHER INFORMATION: Cry3Bb1 variant 11231mv1
; NAME/KEY: terminator
; LOCATION: (3198)..(3431)
; OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-17

Query Match 29.7%; Score 135; DB 4; Length 3450;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 320 TCCTCAGGCTTAGATGTCAGATCTTCTTCTTCTTTGGGAGAAATTGAATCC 379
DB 660 TCCTCAGGCTTAGATGTCAGATCTTCTTCTTCTTTGGGAGAAATTGAATCC 719
QY 380 CTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTTGACAATGAGCCTCGTGC 439
DB 720 CTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTTGACAATGAGCCTCGTGC 779
QY 440 GGAGCTTTTGTAG 454
DB 780 GGAGCTTTTGTAG 794
```

```
DB 780 GGAGCTTTTGTAG 794

RESULT 12
US-09-377-466B-36
; Sequence 36, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 3455
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: promoter
; LOCATION: (14)..(235)
; OTHER INFORMATION: P-CaMV.AS4
; NAME/KEY: 5'UTR
; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: Intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Os.Act1
; NAME/KEY: transit peptide
; LOCATION: (825)..(971)
; OTHER INFORMATION: TS-Zm.rbcs amino terminal coding sequence upstream
; OTHER INFORMATION: of Zea mays rbcs intron
; NAME/KEY: Intron
; LOCATION: (972)..(1134)
; OTHER INFORMATION: I-Zm.rbcs
; NAME/KEY: transit peptide
; LOCATION: (1135)..(1221)
; OTHER INFORMATION: TS-Zm.rbcs carboxy terminus coding sequence
; OTHER INFORMATION: downstream of Zea mays rbcs intron
; NAME/KEY: CDS
; LOCATION: (1222)..(3180)
; OTHER INFORMATION: variant Cry3Bb1 coding sequence encoding v11231
; NAME/KEY: terminator
; LOCATION: (3198)..(3431)
; OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-36

Query Match 29.7%; Score 135; DB 4; Length 3455;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 320 TCCTCAGGCTTAGATGTCAGATCTTCTTCTTCTTTGGGAGAAATTGAATCC 379
DB 660 TCCTCAGGCTTAGATGTCAGATCTTCTTCTTCTTTGGGAGAAATTGAATCC 719
QY 380 CTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTTGACAATGAGCCTCGTGC 439
DB 720 CTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTTGACAATGAGCCTCGTGC 779
QY 440 GGAGCTTTTGTAG 454
DB 780 GGAGCTTTTGTAG 794

RESULT 13
US-09-377-466B-23
; Sequence 23, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
```

```

; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 3469
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: Promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; NAME/KEY: 5'UTR
; LOCATION: (664)..(734)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: Intron
; LOCATION: (748)..(1238)
; OTHER INFORMATION: I-0s.Accl1
; NAME/KEY: CDS
; LOCATION: (1241)..(3199)
; OTHER INFORMATION: Cry3Bb1 variant.11231mv2
; NAME/KEY: terminator
; LOCATION: (3217)..(3450)
; OTHER INFORMATION: T-Ta.hsp17
; US-09-377-466B-23

```

```

Query Match          29.7%; Score 135; DB 4; Length 3469;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      320  TCGTCAGGCTTAAGTGTCTAGATCTTCTTCTTTTGTGGGTAGGAATTGATCC 379
          |||||||
DB      1090  TCGTCAGGCTTAAGTGTCTAGATCTTCTTCTTTTGTGGGTAGGAATTGATCC 1149
          |||||||
QY      380  CTCAGATTGTTGATCGGTAGTTTCTTCTTCATGATTGTGCAATGACGCTCGTGC 439
          |||||||
DB      1150  CTCAGATTGTTGATCGGTAGTTTCTTCTTCATGATTGTGCAATGACGCTCGTGC 1209
          |||||||
QY      440  GGAGCTTTTGTAG 454
          |||||||
DB      1210  GGAGCTTTTGTAG 1224
          |||||||

RESULT 14
US-09-068-101-5
; Sequence 5, Application US/09068101
; Patent No. 6372960
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2121-139P
; CURRENT APPLICATION NUMBER: US/09/068, 101
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: EP 96202446.9
; EARLIER FILING DATE: 1996-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pmw71"
; NAME/KEY: misc feature
; LOCATION: (1995)..(3400)
; OTHER INFORMATION: label = PRACT, "promoter region of rice actin gene

```

```

; OTHER INFORMATION: - contains an intron in the leader"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3401)..(3676)
; OTHER INFORMATION: label = barstar, "barstar DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3677)..(4003)
; OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
; OTHER INFORMATION: T-DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3399)..(3404)
; OTHER INFORMATION: label = NcoI, "NcoI recognition site"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4015)..(4021)
; OTHER INFORMATION: label = KpnI, "KpnI recognition site"
; US-09-068-101-5

```

```

Query Match          29.7%; Score 135; DB 3; Length 4032;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      320  TCGTCAGGCTTAAGTGTCTAGATCTTCTTCTTTTGTGGGTAGGAATTGATCC 379
          |||||||
DB      3259  TCGTCAGGCTTAAGTGTCTAGATCTTCTTCTTTTGTGGGTAGGAATTGATCC 3318
          |||||||
QY      380  CTCAGATTGTTGATCGGTAGTTTCTTCTTCATGATTGTGCAATGACGCTCGTGC 439
          |||||||
DB      3319  CTCAGATTGTTGATCGGTAGTTTCTTCTTCATGATTGTGCAATGACGCTCGTGC 3378
          |||||||
QY      440  GGAGCTTTTGTAG 454
          |||||||
DB      3379  GGAGCTTTTGTAG 3393
          |||||||

```

```

RESULT 15
US-09-970-921-5
; Sequence 5, Application US/09970921
; Patent No. 6758575
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pmw71"
; NAME/KEY: misc feature
; LOCATION: (1995)..(3400)
; OTHER INFORMATION: label = PRACT, "promoter region of rice actin gene
; OTHER INFORMATION: - contains an intron in the leader"
; NAME/KEY: misc feature
; LOCATION: (3401)..(3676)
; OTHER INFORMATION: label = barstar, "barstar DNA"
; NAME/KEY: misc feature
; LOCATION: (3677)..(4003)
; OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
; OTHER INFORMATION: T-DNA"
; NAME/KEY: misc feature
; LOCATION: (3395)..(3404)
; OTHER INFORMATION: label = NcoI, "NcoI recognition site"
; NAME/KEY: misc feature

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 11:40:58 ; Search time 240.829 Seconds
(without alignments)
12380.260 Million cell updates/sec

Title: US-10-758-799-2

Perfect score: 454
Sequence: 1 GTTACACACCCGCCCTCTC.....CGTGGAGCTTTTGTAG 454

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 7351250 seqs, 3283620254 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCUS_NEW_PUB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US10I_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	100.0	454	9	US-09-037-531-2
2	454	100.0	454	19	US-10-758-799-2
3	454	100.0	1565	9	US-09-037-531-3
4	454	100.0	1565	19	US-10-758-799-3
5	291	64.1	623	9	US-09-981-9008-19
6	289	63.7	470	16	US-10-087-167-109
7	203	44.7	1259	10	US-09-991-209-43

8	203	44.7	4773	10	US-09-991-209-32	Sequence 32, Appl
9	203	44.7	4950	10	US-09-991-209-34	Sequence 34, Appl
10	203	44.7	4965	10	US-09-991-209-37	Sequence 37, Appl
11	203	44.7	4974	10	US-09-991-209-35	Sequence 35, Appl
12	203	44.7	5164	10	US-09-991-209-36	Sequence 36, Appl
13	203	44.7	5277	10	US-09-991-209-25	Sequence 25, Appl
14	203	44.7	5295	10	US-09-991-209-38	Sequence 38, Appl
15	203	44.7	5327	10	US-09-991-209-27	Sequence 27, Appl
16	203	44.7	5337	10	US-09-991-209-19	Sequence 19, Appl
17	203	44.7	5337	10	US-09-991-209-23	Sequence 23, Appl
18	203	44.7	5337	10	US-09-991-209-31	Sequence 31, Appl
19	203	44.7	5338	10	US-09-991-209-15	Sequence 15, Appl
20	203	44.7	5338	10	US-09-991-209-29	Sequence 29, Appl
21	203	44.7	5345	10	US-09-991-209-17	Sequence 17, Appl
22	203	44.7	5387	10	US-09-991-209-41	Sequence 41, Appl
23	203	44.7	5395	10	US-09-991-209-21	Sequence 21, Appl
24	135	29.7	491	9	US-09-376-940-50	Sequence 50, Appl
25	135	29.7	1384	22	US-10-839-092-35	Sequence 35, Appl
26	135	29.7	1597	22	US-10-839-092-50	Sequence 50, Appl
27	135	29.7	2460	21	US-10-678-588A-1	Sequence 1, Appl
28	135	29.7	3034	20	US-10-841-796-34	Sequence 34, Appl
29	135	29.7	3039	15	US-10-232-665-19	Sequence 19, Appl
30	135	29.7	3039	15	US-10-232-665-21	Sequence 21, Appl
31	135	29.7	3044	15	US-10-232-665-38	Sequence 38, Appl
32	135	29.7	3450	15	US-10-232-665-17	Sequence 17, Appl
33	135	29.7	3455	15	US-10-232-665-36	Sequence 36, Appl
34	135	29.7	3469	15	US-10-232-665-23	Sequence 23, Appl
35	135	29.7	4032	9	US-09-970-921-5	Sequence 5, Appl
36	135	29.7	5365	22	US-10-839-092-57	Sequence 57, Appl
37	135	29.7	6865	10	US-09-845-064-13	Sequence 13, Appl
38	135	29.7	7794	24	US-11-057-062-2	Sequence 2, Appl
39	135	29.7	7943	10	US-09-845-064-15	Sequence 15, Appl
40	135	29.7	8590	24	US-11-057-062-1	Sequence 1, Appl
41	135	29.7	9143	10	US-09-845-064-12	Sequence 12, Appl
42	135	29.7	9359	21	US-10-344-977A-1	Sequence 1, Appl
43	135	29.7	9359	22	US-10-344-975B-1	Sequence 1, Appl
44	135	29.7	10003	10	US-09-845-064-21	Sequence 21, Appl
45	135	29.7	10003	10	US-09-845-064-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-037-531-2
Sequence 2, Application US/09037531
Patent No. US20020104117A1
GENERAL INFORMATION:
APPLICANT: Derosse, Richard
TITLE OF INVENTION: Freysinet, Georges
TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
TITLE OF INVENTION: And Transformed Plant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Compiloy, Bove, Lodge, & Hutz
STREET: 1220 Market Street
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,531
FILING DATE: 10-MAR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McMorrow Jr., Robert G.
REGISTRATION NUMBER: 30962

```

1      RESULT 2
2      US-10-758-799-2
3      ; Sequence 2, Application US/10758799
4      ; Publication No. US20040199944A1
5      ; GENERAL INFORMATION:
6      ;
7      APPLICANT: DeRose, Richard
8      ;
9      Freysinet, Georges
10     TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
11     First Intron Of Rice Actin, Chimeric Gene Comprising It
12     And Transformed Plant
13     ;
14     ;
15     NUMBER OF SEQUENCES: 5
16     ;
17     CORRESPONDENCE ADDRESS:
18     ;
19     ADDRESSEE: Connolly, Bove, Lodge, & Hutz
20     ;
21     STREET: 1220 Market Street
22     ;
23     CITY: Wilmington
24     ;
25     STATE: DE
26     ;
27     COUNTRY: USA
28     ;
29     ZIP: 19899
30     ;
31     COMPUTER READABLE FORM:
32     ;
33     MEDIUM TYPE: Floppy disk
34     ;
35     COMPUTER: IBM PC compatible
36     ;
37     OPERATING SYSTEM: PC-DOS/MS-DOS
38     ;
39     SOFTWARE: PatentIn Release #1.0, Version #1.25
40     ;
41     CURRENT APPLICATION DATA:
42     ;

```

```

1  RESULT 3
2  US-09-037-531-3
3  ; Sequence 3, Application US/09037531
4  ; Patent No. US20020104117A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Derose, Richard
7  ; APPLICANT: Freysinet, Georges
8  ; TITLE OF INVENTION: Mzize H3c4 Promoter Combined With The
9  ; TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
10 ; TITLE OF INVENTION: And Transformed Plant
11 ; NUMBER OF SEQUENCES: 5
12 ; CORRESPONDENCE ADDRESSES:
13 ; ADDRESSEE: Connolly, Boyle, Lodge, & Hutcz
14 ; STREET: 1220 Market Street

```


Query Match	64.1%;	Score 291;	DB 9;	Length 623;
Best Local Similarity	100.0%;	Pred. No. 2.3e-139;		
Matches 291;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

ESULT 6
S-10-087-167-109

ORGANISM: *Oryza sp.*
S-10-087-167-109

Qy	166	GGATCTCGCGGGAAATGGGGCTCTCGGATGTAAATCGATCGCGCGTTGTGGGGAGAGA	225
Db	166	GGATCTCTCGCGGGAAATGGGGCTCTCGGATGTAAATCGATCGCGCGTTGTGGGGAGAGA	225
Qy	226	TGATGGGGCGTTAAAAATTTCCGATGCTAAACAAGATCAGAGAGAGGGGAAAAAGGGCAC	285
Db	226	TGATGGGGCGCTTAAAAATTTCCGATGCTAAACAAGATCAGAGAGAGGGGAAAAAGGGCAC	285
Qy	286	TATGTTTAATTTTATATATATTTCTGCTGCTGCGTCGTCAGAGCTAAGATGACTGATCT	345
Db	286	TATGTTTAATTTTATATATATTTCTGCTGCTGCGTCGTCAGAGCTAAGATGACTGATCT	345
Qy	346	TTCTTTCTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTGTTCAATCGGTAGTTTTT	405
Db	346	TTCTTTCTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTGTTCAATCGGTAGTTTTT	405
Qy	406	CTTTTCATGATTTGTGACCAATGAGAGCTCGTGGCGAGACTTTTGTGTAG	454
Db	406	CTTTTCATGATTTGTGACCAATGAGAGCTCGTGGCGAGACTTTTGTGTAG	454

Query Match	44.7%;	Score 203;	DB 10;	Length 1259;
Best Local Similarity	100.0%;	Pred. No. 5.4e-94;		
Matches 203;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]


```

? TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
? FILE REFERENCE: GC648-2
? CURRENT APPLICATION NUMBER: US/09/991,209
? CURRENT FILING DATE: 2002-07-02
? PRIOR APPLICATION NUMBER: US 60/249,608
? PRIOR FILING DATE: 2000-11-17
? NUMBER OF SEQ ID NOS: 97
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 38
? LENGTH: 5295
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: pUG4 vector
? US-09-991-209-38

```

Query Match	44.7%;	Score 203;	DB 10;	length 5295;
Best Local Similarity	100.0%;	Pred. No. 5.6e-94;		
Matches 203; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

61 CTTTGGCCCTTGTGATTTGGGTGGGCGAAGCGCGCTTCGTGCGCCAGATCGTGC CGCGG 120
5041 CTTTGGCCCTTGTGATTTGGGTGGGCGAAGCGCGCTTCGTGCGCCAGATCGTGC CGCGG 5100

QY 121 AGGGGCGGATCTCGCGCTGCGCGTCTCCGGGCGTAGTTCGCCGGATCTCCGGGGA 180

Db 5101 AGGGGCGGATCTCGCGCTGCGCGTCTCCGGGCGTAGTTCGCCGGATCTCTCCGGGGA 5160

QY	181	ATGGGGCTCTGGAGTAGATCT	203
Db	5161	ATGGGGCTCTGGAGTAGATCT	5183

RESULT 15
US-09-991

```

Sequence 27 Application US/05991209
Publication No. US20030024009A1
GENERAL INFORMATION:
APPLICANT: Dunn-Coleman, Nigel
APPLICANT: Langdon, Timothy
APPLICANT: Morse, Philip
TITLE OF INVENTION: Manipulation of the Phenolic Acid
TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
FILE REFERENCE: G0448-2
CURRENT APPLICATION NUMBER: US/05/991,209
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/249,608
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 5327
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pTP4a2 vector
US-09-991-209-27

```

Query Match	44.7%;	Score 203;	DB 10;	Length 5327;
Best Local Similarity	100.0%;	Pred. No. 5.6e-94;		
Matches 203; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Gy	1 GTAAACACCCCGGCCCTCTCCTCTTCTTCGTTTTTTTGCTCGGTCTCAT	60
Dd	4789 GTAAACACCCCGGCCCTCTCCTCTTCTTCGTTTTTTTGCTCGGTCTCAT	4848

61 CTTTGGCCCTTGCTAGTTGGGTGGCCAGAGCGGCTTCGTCCGCCAGATCGGTGCGCGGG 120

Db	4849	CTTGGCCCTTGAGTTGGATGGGACAGACGGCTTCGTCGCCAATCGATCGATCGCGG	4908
Oy	121	AGGGGCGGGATCTCGCGGCTGCGCTCTCCGGGCGTAGTGGGCCCGGATCTCGCGGG	180
Db	4909	AGGGGCGGGATCTCGCGGCTGCGCTCTCCGGGCGTAGTGGGCCCGGATCTCGCGGG	4968
Oy	181	ATGGGGCTTCGGATTGAGTCT	203
Db	4969	ATGGGGCTTCGGATTGAGTCT	4991

Search completed: September 12, 2005, 16:58:29
Job time : 242.829 secs

THIS PAGE BLANK (USPTO)

Db 181 TTTCTCATATTTTTCCTTATACATTTTGGGCTTACATTCATCATATATATCA 240
 QY 241 TCTTTCCGGTGTCTCTAATAAGATTCATCTCTGAATTTTCTCTCCAAATACGT 300
 Db 241 TCTTTCCGGTGTCTCTAATAAGATTCATCTCTGAATTTTCTCTCCAAATACGT 300
 QY 301 TCTCTAATCAGGTCTCTAATAGCAATACCTATTATAGAGACATTTTATTTTGTAC 360
 Db 301 TCTCTAATCAGGTCTCTAATAGCAATACCTATTATAGAGACATTTTATTTTGTAC 360
 QY 361 ATACATATTTGTCAATCTCTCAATGCAATATACATATTTAGTTTATCAACCGATAT 420
 Db 361 ATACATATTTGTCAATCTCTCAATGCAATATACATATTTAGTTTATCAACCGATAT 420
 QY 421 TTTAATGATTTCAACCGATAGAACTGTTATAGTAATTTCTATATATAGAAATCCAGT 480
 Db 421 TTTAATGATTTCAACCGATAGAACTGTTATAGTAATTTCTATATATAGAAATCCAGT 480
 QY 481 AGCGTCTCTAATTTAGATGATTTATTTAGAGACGCTGTAGAAAAAGTAAATTTCT 540
 Db 481 AGCGTCTCTAATTTAGATGATTTATTTAGAGACGCTGTAGAAAAAGTAAATTTCT 540
 QY 541 TTGATTTATTTATTTAGGTTAGAGTAGACCTTTATGCTTTATAGATCTTTGTGACCA 600
 Db 541 TTGATTTATTTATTTAGGTTAGAGTAGACCTTTATGCTTTATAGATCTTTGTGACCA 600
 QY 601 GCGTTATACCGGTTATTTTGGCAATGGCGCTCTCATTTTCTACCCAGCGCCCAATTT 660
 Db 601 GCGTTATACCGGTTATTTTGGCAATGGCGCTCTCATTTTCTACCCAGCGCCCAATTT 660
 QY 661 TCACGTTTTTCAACGGAAGCGCCAGCGCTTAAACCAATTTGTATCGGTGGCGGTT 720
 Db 661 TCACGTTTTTCAACGGAAGCGCCAGCGCTTAAACCAATTTGTATCGGTGGCGGTT 720
 QY 721 TTCAAAAGAGTGGAAACCATCTGCAACCCAGCATAGAGCCCTCGGATCTTCCCTG 780
 Db 721 TTCAAAAGAGTGGAAACCATCTGCAACCCAGCATAGAGCCCTCGGATCTTCCCTG 780
 QY 781 ATTAAATCTTACGCAATAGAGCCCAAGACCAACCATCAAGCGGATGTCTTACGCTTC 840
 Db 781 ATTAAATCTTACGCAATAGAGCCCAAGACCAACCATCAAGCGGATGTCTTACGCTTC 840
 QY 841 CACCTCATGGGCGCGCTCATCTCAACCAACCTATTGCTTACCTTGGCCATCTCC 900
 Db 841 CACCTCATGGGCGCGCTCATCTCAACCAACCTATTGCTTACCTTGGCCATCTCC 900
 QY 901 GAAAAAATTTCTCGGCTTCCGCTCCGCACTTAACTAATCCATCCCATCAAGCGCAT 960
 Db 901 GAAAAAATTTCTCGGCTTCCGCTCCGCACTTAACTAATCCATCCCATCAAGCGCAT 960
 QY 961 CGCATCACTGCAAAATCCCAAGAAATTAAGCCGCAACCGCTTCCAGCTGCCAACAAT 1020
 Db 961 CGCATCACTGCAAAATCCCAAGAAATTAAGCCGCAACCGCTTCCAGCTGCCAACAAT 1020
 QY 1021 CGCGCTCTCCGCGCAAGCAACCAAGAAATTTGCGCGCAACCGGCGGTGAGCTCTCC 1080
 Db 1021 CGCGCTCTCCGCGCAAGCAACCAAGAAATTTGCGCGCAACCGGCGGTGAGCTCTCC 1080
 QY 1081 CTTCCCTCTCCGCGCGCGGATACCAACCCGCGCTCTCTCTTTCTTCTCGTTTT 1140
 Db 1081 CTTCCCTCTCCGCGCGCGGATACCAACCCGCGCTCTCTCTTTCTTCTCGTTTT 1140
 QY 1141 TTTTTCGTCTCGGCTCTCAATCTTTTGGCTTTGGATTTTGGTGGGAGAGCGGCTTG 1200
 Db 1141 TTTTTCGTCTCGGCTCTCAATCTTTTGGCTTTGGATTTTGGTGGGAGAGCGGCTTG 1200
 QY 1201 TGCCCAAGATCGGTGGCGGGAAGGAGGAGATCTCGGCGGTGAGTCCGGCGGTGAGT 1260
 Db 1201 TGCCCAAGATCGGTGGCGGGAAGGAGGAGATCTCGGCGGTGAGTCCGGCGGTGAGT 1260
 QY 1261 CGGCGCGGATCTCTCGGCGGAATGGGGCTCTCGGATGTAGATCTGATCCGCGTGTGG 1320
 Db 1261 CGGCGCGGATCTCTCGGCGGAATGGGGCTCTCGGATGTAGATCTGATCCGCGTGTGG 1320

Db 1261 CGGCGCGGATCTCTCGGCGGAATGGGGCTCTCGGATGTAGATCTGATCCGCGTGTGG 1320
 QY 1321 GGAAGATGATGGGGGTTTAAATTTCCGCAATGCTAAACAAGATCGAAGAGGGAATA 1380
 Db 1321 GGAAGATGATGGGGGTTTAAATTTCCGCAATGCTAAACAAGATCGAAGAGGGAATA 1380
 QY 1381 GGGCACTATGTTTATTTTATTTATTTATTTTCTGCTGCTGCTGAGGCTTATGATGTCT 1440
 Db 1381 GGGCACTATGTTTATTTTATTTATTTATTTTCTGCTGCTGCTGAGGCTTATGATGTCT 1440
 QY 1441 AGATCTTTCTTTCTTTTCTTTTGTGGTAGAATTTGAATCCCTCAGCATTTGTCATCGTA 1500
 Db 1441 AGATCTTTCTTTCTTTTGTGGTAGAATTTGAATCCCTCAGCATTTGTCATCGTA 1500
 QY 1501 GTTTTCTTTTATGATTTTGTGCAAAATGACGCTGTGGGAGGCTTTTGTAGATAGA 1560
 Db 1501 GTTTTCTTTTATGATTTTGTGCAAAATGACGCTGTGGGAGGCTTTTGTAGATAGA 1560
 QY 1561 CCATG 1565
 Db 1561 CCATG 1565
 RESULT 2
 AR559745
 LOCUS AR559745 1565 bp DNA linear PAT 08-OCT-2004
 DEFINITION Sequence 3 from patent US 6750378.
 ACCESSION AR559745
 VERSION AR559745.1 GI:53969843
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 1565)
 AUTHORS Derose, R. and Freysbinder, G.
 TITLE Maize H3C4 promoter combined with the first intron of rice actin,
 chimeric gene comprising it and transformed plant
 JOURNAL Patent: US 6750378-A 3 15-JUN-2004;
 FEATURES
 source location/Qualifiers
 1..1565
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Query Match 100.0%; Score 1565; DB 6; Length 1565;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAATTCCTGCAAGTGCAGCGATCCCTTATGTGACCACTTTACTGTATGATATCAT 60
 Db 1 GAATTCCTGCAAGTGCAGCGATCCCTTATGTGACCACTTTACTGTATGATATCAT 60
 QY 61 TTAATTTGAATAGCAAACTTTTCTATTTACTTCTTTACTTAACTAATTTCTGTTTAAAT 120
 Db 61 TTAATTTGAATAGCAAACTTTTCTATTTACTTCTTTACTTAACTAATTTCTGTTTAAAT 120
 QY 121 TCAGTCTCTCAATTCATTTGCTCAAGTAAATTTGAGACTGTCAAAATTTTATTTTAT 180
 Db 121 TCAGTCTCTCAATTCATTTGCTCAAGTAAATTTGAGACTGTCAAAATTTTATTTTAT 180
 QY 181 TTCTTCATATTTTTCCTTATATACATTTTGGGCTTTACATTCATCATCTATATCA 240
 Db 181 TTCTTCATATTTTTCCTTATATACATTTTGGGCTTTACATTCATCATCTATATCA 240
 QY 241 TCTTTTCGGGTGTCTCTAATAAGATTCATCTCTGAATCTTATTCCTTCAATATACGT 300
 Db 241 TCTTTTCGGGTGTCTCTAATAAGATTCATCTCTGAATCTTATTCCTTCAATATACGT 300
 QY 301 TCTCTAATCAGGTCTCTAATAGCAATACCTATTATAGAGACATTTTATTTTGTAC 360
 Db 301 TCTCTAATCAGGTCTCTAATAGCAATACCTATTATAGAGACATTTTATTTTGTAC 360
 QY 361 ATACATATTTGTCAATCTCTCAATGCAATATATATATATTTAGTTTACTTAAACGATAT 420


```

Db      361 ATACATTTTGTCTACTCTCAATGATATATATATTTAGTTTACTTAACCGATAT 420
Qy      421 TTAAGTATTCAAACGAGTGAAGAACTGTTTAAATAATTCATATATAGAAATCCAGT 480
Db      421 TTAAGTATTCAAACGAGTGAAGAACTGTTTAAATAATTCATATATAGAAATCCAGT 480
Qy      481 AGGTTCTCTAAATTTTATGATATTTATAGAGACGCTGTAAATAACGTAATAATTC 540
Db      481 AGGTTCTCTAAATTTTATGATATTTATAGAGACGCTGTAAATAACGTAATAATTC 540
Qy      541 TTGATTATTTATTTAGGTAGAGTACCTTTATGCTTATATAGATCTTTGTGACCA 600
Db      541 TTGATTATTTATTTAGGTAGAGTACCTTTATGCTTATATAGATCTTTGTGACCA 600
Qy      601 GCCTTATACCGTATTTTTCGCAATGCGCTCTCATTTTCACTCCAGCCGCCACATTT 660
Db      601 GCCTTATACCGTATTTTTCGCAATGCGCTCTCATTTTCACTCCAGCCGCCACATTT 660
Qy      661 TCAGTTTTCACGAAAGCGCCAGCCTGCTTAACCAAAATTTGTAACGTTGGCGGTT 720
Db      661 TCAGTTTTCACGAAAGCGCCAGCCTGCTTAACCAAAATTTGTAACGTTGGCGGTT 720
Qy      721 TTCAAAAGAGTGGAAACCATCTGCAACGACGACGACGACGACGACGACGACGACG 780
Db      721 TTCAAAAGAGTGGAAACCATCTGCAACGACGACGACGACGACGACGACGACGACG 780
Qy      781 ATTAAGTCTTAGCCAAATAGAGGCCAGAAACCAACCATCAAGCGAGATGCTTACGCTTC 840
Db      781 ATTAAGTCTTAGCCAAATAGAGGCCAGAAACCAACCATCAAGCGAGATGCTTACGCTTC 840
Qy      841 CACCTCATCGGCGCGCTCCATCTCCATCAACACTATTCGTTACCTTGCCATCTCTCC 900
Db      841 CACCTCATCGGCGCGCTCCATCTCCATCAACACTATTCGTTACCTTGCCATCTCTCC 900
Qy      841 CACCTCATCGGCGCGCTCCATCTCCATCAACACTATTCGTTACCTTGCCATCTCTCC 900
Db      901 GAAAAAATTCCTGGGCTCGGCTCCGCACTACCAATACCAATCCATCCATCAAGAGCAT 960
Qy      901 GAAAAAATTCCTGGGCTCGGCTCCGCACTACCAATACCAATCCATCCATCAAGAGCAT 960
Db      901 GAAAAAATTCCTGGGCTCGGCTCCGCACTACCAATACCAATCCATCCATCAAGAGCAT 960
Qy      961 CGCATCACTGCGCAAAATCCCGCAAAATCAACACTTCCCAATTCACGCTGCCACCAACT 1020
Db      961 CGCATCACTGCGCAAAATCCCGCAAAATCAACACTTCCCAATTCACGCTGCCACCAACT 1020
Qy      1021 CGCGCTCTCCGCGCCAGCAACCAAGAAATGCGCGCCACCGCGGTGAGCTCTCC 1080
Db      1021 CGCGCTCTCCGCGCCAGCAACCAAGAAATGCGCGCCACCGCGGTGAGCTCTCC 1080
Qy      1081 CTTCCCTCCGCGCGCGCGCGGTAACCAACCCCGCTCTCTCTCTCTCTCTCTCTCTCT 1140
Db      1081 CTTCCCTCCGCGCGCGCGCGGTAACCAACCCCGCTCTCTCTCTCTCTCTCTCTCTCT 1140
Qy      1141 TTTTTCCTGCTCGGCTCTCGATCTTTGCTTGGAGTTGGGTGGGAGAGCGGCTTCG 1200
Db      1141 TTTTTCCTGCTCGGCTCTCGATCTTTGCTTGGAGTTGGGTGGGAGAGCGGCTTCG 1200
Qy      1201 TCGCCAGATCGGTGCGCGGAGCGGAGCTCTCGGCTGCGCTCTCGGCGCTGAGT 1260
Db      1201 TCGCCAGATCGGTGCGCGGAGCGGAGCTCTCGGCTGCGCTCTCGGCGCTGAGT 1260
Qy      1261 CGGCGCGGATCTCTCGCGGGAATGGGGCTCTCGGATGTAGATCTGATCCGCGTGTGG 1320
Db      1261 CGGCGCGGATCTCTCGCGGGAATGGGGCTCTCGGATGTAGATCTGATCCGCGTGTGG 1320
Qy      1321 GGGAGATGATGGGCGGTTTAAATTTGCGCATGCTAAACAAGATCAGAGAAGAGGGGAAA 1380
Db      1321 GGGAGATGATGGGCGGTTTAAATTTGCGCATGCTAAACAAGATCAGAGAAGAGGGGAAA 1380
Qy      1381 GGGAGATGATGGGCGGTTTAAATTTGCGCATGCTAAACAAGATCAGAGAAGAGGGGAAA 1440
Db      1381 GGGAGATGATGGGCGGTTTAAATTTGCGCATGCTAAACAAGATCAGAGAAGAGGGGAAA 1440
Qy      1441 AGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1500

```

```

Db      1441 AGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1500
Qy      1501 GTTTTCTTTTCATGATTTTGTGACAAATGCAAGCTTGTGCGAGCTTTTGTAGGTAA 1560
Db      1501 GTTTTCTTTTCATGATTTTGTGACAAATGCAAGCTTGTGCGAGCTTTTGTAGGTAA 1560
Qy      1561 CCATG 1565
Db      1561 CCATG 1565

RESULT 3
BD128391
LOCUS   BD128391
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1565)
AUTHORS
Durose, R. and Freyslet, G.
TITLE
CORN H3C4 PROMOTER BONDED TO THE FIRST INTRON OF RICE ACTIN,
JOURNAL
chimeric gene containing this promoter and transgenic plant
PATENT: JP 2002500016-A/3
COMMENT
OS
PN
JP 2002500016-A/3
PE
22-DEC-1998 JP 2000526660
PR
24-DEC-1997 FR 97/16726
PI
RICHARD DUROSE, GEORGES FREYSLET
PC
C12N15/09, A01H5/00, C07K14/21, C07K14/415, C07K19/00, C12N5/10, PC
C12Q1/68
PC
C12N15/00, C12N5/00
CC
Strandedness: Single;
CC
Topology: Linear;
CC
CORN H3C4 PROMOTER BONDED TO THE FIRST INTRON OF RICE ACTIN,
CC
chimeric gene
CC
containing this promoter and transgenic plant
FT
Location/Qualifiers
FT
source
1..1565
/organism='Unidentified'.
FEATURES
source
1..1565
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 1565; DB 6; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GAATTCCTGCAAGTTCAGATCCCTTATGTGACCAATTTACTGTAAATGCAATATCAT 60
Db      1 GAATTCCTGCAAGTTCAGATCCCTTATGTGACCAATTTACTGTAAATGCAATATCAT 60
Qy      61 TTAATGAAATAGCAAACTTTTCTATTAATCTTTTACTAACATTAATCTTGTTTAAAT 120
Db      61 TTAATGAAATAGCAAACTTTTCTATTAATCTTTTACTAACATTAATCTTGTTTAAAT 120
Qy      121 TCAGTCTCAACATTCATGCTCAAGTATAGTGTGAGCTGTCAAAATTTACTATTTTAT 180
Db      121 TCAGTCTCAACATTCATGCTCAAGTATAGTGTGAGCTGTCAAAATTTACTATTTTAT 180
Qy      181 TTCTTCATATTTTCTTTCTTTATATACATTTTGGGCTTAAATCATCATATATATATCA 240
Db      181 TTCTTCATATTTTCTTTCTTTATATATATATATATATATATATATATATATATATCA 240
Qy      241 TCCCTTCGCGGTGCTCTAAAGATTCATCCCTGATGATCTTATTCCTCCAAATACGT 300

```

Db 241 TCCCTTCCGAGTGCCTCTAAAGATTCATCCCTCAATCTTATCTCCCAATACGT 300
 QY 301 TCCCTTAATCAGGTCCTTAATGACATPACATATATATAGAGACATTTTTTATTTTGTAC 360
 Db 301 TCTCTAAATCAGGTCCTTAATGACATPACATATATATAGAGACATTTTTTATTTTGTAC 360
 QY 361 ATACATATTTTGTATCTCTCAATGCAATATATACATATTTAGTTTACTTAACCGATAT 420
 Db 361 ATACATATTTTGTATCTCTCAATGCAATATATACATATTTAGTTTACTTAACCGATAT 420
 QY 421 TTAAGATTTCAACCGATGAGAACTGTTAGATAAATTCTATATATATAGAGATCCAGT 480
 Db 421 TTAAGATTTCAACCGATGAGAACTGTTAGATAAATTCTATATATAGAGATCCAGT 480
 QY 481 AGCGTCTCTAAATTTAGATTTATTTAGAGAGACCGCTGTAAAGAAACGTAAGAAATTCG 540
 Db 481 AGCGTCTCTAAATTTAGATTTATTTAGAGAGACCGCTGTAAAGAAACGTAAGAAATTCG 540
 QY 541 TTGATTTATTTATTTAGGATAGTAGCTTTATGCTTTATAGATCTTTGTGTAGACCA 600
 Db 541 TTGATTTATTTATTTAGGATAGTAGCTTTATGCTTTATAGATCTTTGTGTAGACCA 600
 QY 601 GCCTTATACCGGTTATTTTTCGCAATGCGCTCTCATTTTCACTCAAGCGCCCACTTT 660
 Db 601 GCCTTATACCGGTTATTTTTCGCAATGCGCTCTCATTTTCACTCAAGCGCCCACTTT 660
 QY 661 TCACGTTTTCACGAGAGCGCCGAGCTGCTTAACCAAAATTTGTATCGGTGCGGGGT 720
 Db 661 TCACGTTTTCACGAGAGCGCCGAGCTGCTTAACCAAAATTTGTATCGGTGCGGGGT 720
 QY 721 TTCAAAAGAGTGGAAACCATCTGACCCACGAGTATGAGGCGCTCGGATCTCTCTG 780
 Db 721 TTCAAAAGAGTGGAAACCATCTGACCCACGAGTATGAGGCGCTCGGATCTCTCTG 780
 QY 781 ATTAAGTCTTAAGCAATAGAGCCCAAGAACCACTTACGCGGATGCTCTTACGCTTC 840
 Db 781 ATTAAGTCTTAAGCAATAGAGCCCAAGAACCACTTACGCGGATGCTCTTACGCTTC 840
 QY 841 CACCTCATGCGGCGCGCTCATCTCAACCAACCTTACGCTTACGCTTACGCTTACGCT 900
 Db 841 CACCTCATGCGGCGCGCTCATCTCAACCAACCTTACGCTTACGCTTACGCTTACGCT 900
 QY 901 GAAAAAATCTCGGCTCGCGCTCCGACCTTACTCAAAATCCATCCATCAGACGCAAT 960
 Db 901 GAAAAAATCTCGGCTCGCGCTCCGACCTTACTCAAAATCCATCCATCAGACGCAAT 960
 QY 961 CGCATCACTGCAAAATCCCAAGAAATCAACCTTCCCAATTCACGCTGCCACCAACT 1020
 Db 961 CGCATCACTGCAAAATCCCAAGAAATCAACCTTCCCAATTCACGCTGCCACCAACT 1020
 QY 1021 CGCGGCTCTCCGCGGCAAGACCAAAAGAAATTTGCGGCGCACGCGGTTGAGGCTCTCC 1080
 Db 1021 CGCGGCTCTCCGCGGCAAGACCAAAAGAAATTTGCGGCGCACGCGGTTGAGGCTCTCC 1080
 QY 1081 CCGCCCGCTCGCGCGCGCGGATACCAACCCGCGCTCTCTCTTTCTTCTCCGTTT 1140
 Db 1081 CCGCCCGCTCGCGCGCGCGGATACCAACCCGCGCTCTCTCTTTCTTCTCCGTTT 1140
 QY 1141 TTTTTCGCTCGGCTCGATCTTTTGGCTTTGAGTTTGGTGGGAGAGCGGCTTCG 1200
 Db 1141 TTTTTCGCTCGGCTCGATCTTTTGGCTTTGAGTTTGGTGGGAGAGCGGCTTCG 1200
 QY 1201 TCGCCCAAGATCGGATGCGGAGAGGCGGAGATCTCGGCGCTGCGCTCCGCGGCGTGA 1260
 Db 1201 TCGCCCAAGATCGGATGCGGAGAGGCGGAGATCTCGGCGCTGCGCTCCGCGGCGTGA 1260
 QY 1261 CGGCGCGGATCTCTCGCGGGAATGAGGCTCTCGGATGTAGATCTGATCCGCGTTGTG 1320
 Db 1261 CGGCGCGGATCTCTCGCGGGAATGAGGCTCTCGGATGTAGATCTGATCCGCGTTGTG 1320
 QY 1321 GGGAGATGATGGGCGTTTAAATTTTCGCAATCTAAACAAATCATGAGAAAGAGGGA 1380
 Db 1321 GGGAGATGATGGGCGTTTAAATTTTCGCAATCTAAACAAATCATGAGAAAGAGGGA 1380

Db 1321 GGGAGATGATGGGCGTTTAAATTTGCCATGCTTAAACAAATCATGAGAAAGAGGGA 1380
 QY 1381 GGGACATAGTGTATTTATTTATATTTTCTGCTGCTGCTGATGAGTGTCT 1440
 Db 1381 GGGACATAGTGTATTTATTTATATTTTCTGCTGCTGCTGATGAGTGTCT 1440
 QY 1441 AGATCTTTCTTTCTTTTGTGGTGAATTTGAATTCCTCAGCATTTGTTCAATCGGTA 1500
 Db 1441 AGATCTTTCTTTCTTTTGTGGTGAATTTGAATTCCTCAGCATTTGTTCAATCGGTA 1500
 QY 1501 GTTTTCTTTTCAATATTTGACAAATGCGAGCTCGGAGGCTTTTGTAGGTAGA 1560
 Db 1501 GTTTTCTTTTCAATATTTGACAAATGCGAGCTCGGAGGCTTTTGTAGGTAGA 1560
 QY 1561 CCATG 1565
 Db 1561 CCATG 1565
 RESULT 4
 A94723 1021 bp DNA linear PAT 26-JAN-2000
 LOCUS A94723
 DEFINITION Sequence 1 from Patent WO9934005.
 ACCESSION A94723
 VERSION A94723.1 GI:678988
 KEYWORDS
 SOURCE
 ORGANISM
 unidentifed
 unclassified.
 1 (bases 1 to 1021)
 REFERENCE
 Derose,R. and Freysstine,G.
 MAIZE H3C4 PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON,
 CHIMERIC GENE CONTAINING IT AND TRANSFORMED PLANT
 Patent: WO 9934005-A 1 08-JUL-1999;
 JOURNAL
 RHOBE POULENC AGROCHIMIE (FR)
 FEATURES
 source
 1..1021
 /organism="unidentifed"
 /mol_type="unasigned DNA"
 /db_xref="taxon:32644"
 1..1021
 ORIGIN
 Promoter
 Query Match 65.2%; Score 1021; DB 6; Length 1021;
 Best Local Similarity 100.0%; Pred. No. 1.7e-208;
 Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 CTTATGTGACCATTTACTGTATGATCATATTTAATTTGATAGCAACTTTTCTATT 86
 Db 1 CTTATGTGACCATTTACTGTATGATCATATTTAATTTGATAGCAAACTTTTCTATT 60
 QY 87 ACTTCCTTAATCAATTAATCTTGGTTTAAATCAAGCCCAACATTCATGCTCAAG 146
 Db 61 ACTTCCTTAATCAATTAATCTTGGTTTAAATCAAGCCCAACATTCATGCTCAAG 120
 QY 147 TATTAAGTGAAGCTGCAAAATTTACTATTTTATTTCTTCATATTTTTCCTATACA 206
 Db 121 TATTAAGTGAAGCTGCAAAATTTACTATTTTATTTCTTCATATTTTTCCTATACA 180
 QY 207 CATTTTGGGCTTAACATTCATATCATATTCATTCCTTCCGGTGTCTCTAAAAGATT 266
 Db 181 CATTTTGGGCTTAACATTCATATCATATTCATTCCTTCCGGTGTCTCTAAAAGATT 240
 QY 267 CCATCCTCGAATCTTATTCCTCGCAATTAACGTCCTGAATTCAGTCTATTAAGCA 326
 Db 241 CCATCCTCGAATCTTATTCCTCGCAATTAACGTCCTGAATTCAGTCTATTAAGCA 300
 QY 327 TACCTATATTAAGACATTTTATTTTATTTTGTACATATTTGTCACTACTCAATG 386
 Db 301 TACCTATATTAAGACATTTTATTTTATTTTGTACATATTTGTCACTACTCAATG 360
 QY 387 CATTAATCATATTTAGTTTACTTAAACGATTTATTTAAATGATTCAAACGATGAAGAC 446
 Db 387 CATTAATCATATTTAGTTTACTTAAACGATTTATTTAAATGATTCAAACGATGAAGAC 446

Db	361	CATTATATCATATTAGTTTACTTAACCCGATTTATTTAAAGTTCAAACGATGAAGAC	420
Qy	447	TGTTTAGATAAAATCTATATATAGAAATCCAGTAGCGTCTCTAAATTTAGATGATTAT	506
Db	421	TGTTTAGATAAAATCTATATATAGAAATCCAGTAGCGTCTCTAAATTTAGATGATTAT	480
Qy	507	TTAAGAGACGCTGTTAGAAAACGTAATAAAATTTCTTGATTTATTTATTTAGGGTAGAGT	566
Db	481	TTAAGAGACGCTGTTAGAAAACGTAATAAAATTTCTTGATTTATTTATTTAGGGTAGAGT	540
Qy	567	AGCCTTTATGCTTTATATAGATCTTTGGTAGACCCAGCCCTATACCGGTTATTTTGGCATT	626
Db	541	AGCCTTTATGCTTTATATAGATCTTTGGTAGACCCAGCCCTATACCGGTTATTTTGGCATT	600
Qy	627	GCGCCTCTCATTTTTCACCTCCAGACGCGCCACATTTTTCACGTTTTCACCGAAGCGCCAGCC	686
Db	601	GCGCCTCTCATTTTTCACCTCCAGACGCGCCACATTTTTCACGTTTTCACCGAAGCGCCAGCC	660
Qy	687	TGCTTAACCAACAAATTTGTTACGTTGCGCGCGGTTTTCAAAAGAAAGTGGAAACCATCTGC	746
Db	661	TGCTTAACCAACAAATTTGTTACGTTGCGCGCGGTTTTCAAAAGAAAGTGGAAACCATCTGC	720
Qy	747	ACCCACCGACATGATAGAGCGCCCTCGATCTCTCTGATTAATGTCCTAATGCCAATAGAGACCC	806
Db	721	ACCCACCGACATGATAGAGCGCCCTCGATCTCTCTGATTAATGTCCTAATAGAGAGACCC	780
Qy	807	GAACCAACCCATCATACGCGGATGTCGCTTACGCTTCCACTCATTCATCGGCGCGCTCATCTCCA	866
Db	781	GAACCAACCCATCATACGCGGATGTCGCTTACGCTTCCACTCATTCATCGGCGCGCTCATCTCCA	840
Qy	867	TCCAAACACCTATTCGTTACCTTGGCCATCTCCGAAAAAATTCGCGCTCGCGCTCGCG	926
Db	841	TCCAAACACCTATTCGTTACCTTGGCCATCTCCGAAAAAATTCGCGCTCGCGCTCGCG	900
Qy	927	ACCTAATCTCAAAATACCCATCTCCATATAGACGATGTCATCTGCGAAATCCCCCAAAA	986
Db	901	ACCTAATCTCAAAATACCCATCTCCATATAGACGATGTCATCTGCGAAATCCCCCAAAA	960
Qy	987	ATCAACACCTCCCAATTTCCAGCGTGCACCAACTGCGCGTCTCGCGCGCAAGCACCAAA	1046
Db	961	ATCAACACCTCCCAATTTCCAGCGTGCACCAACTGCGCGTCTCGCGCGCAAGCACCAAA	1020
Qy	1047	G 1047	
Db	1021	G 1021	
RESULT 5			
LOCUS	ARS59743	1021 bp	DNA linear PAT 08-OCT-2004
DEFINITION	Sequence 1 from patent US 6750378.		
ACCESSION	ARS59743		
VERSION	ARS59743.1	GI:53969841	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1021)		
TITLE	Derose,R. and Freysinet,G.		
JOURNAL	Maize H3C4 promoter combined with the first intron of rice actin,		
FEATURES	Chimeric gene comprising it and transformed plant		
source	Patent: US 6750378-A 1 15-JUN-2004;		
	Location/Qualifiers		
	1..1021		
ORIGIN	/Organism="Unknown"		
	/mol_type="genomic DNA"		
Query Match	55.2%; Score 1021; DB 6; Length 1021;		
Best Local Similarity	100.0%; Pred. No. 1.7e-208;		
Matches 1021; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
Qy	27	CTTAGTGCACCATTTACTGTAAATGCATATCATTTAATGAATAGCAAACTTTTCTATT	86

Db	1	CTTATGTCACCATTTACTGTAAATGCATTAATCATTTTAATGATAGCAAACTTTTCTAATT	60
Qy	87	ACCTCTTTACTAACAATAATCTTGTTTTAAATTTCAAGTCTCTCAACATTCATGCTCAAG	146
Db	61	ACTCTTTACTAACAATAATCTTGTTTTAAATTTCAAGTCTCTCAACATTCATGCTCAAG	120
Qy	147	TATAAGTTAGACGTGTCAAAATTTACTAATTTAATTTCTCATATTTTTTTCCTTAATCA	206
Db	121	TATAAGTTAGACGTGTCAAAATTTACTAATTTAATTTCTCATATTTTTTTCCTTAATCA	180
Qy	207	CATTTTGGGCGCTTAACATTCATCATTAATTCATCTTCGCGGTCCCTTAAGATT	266
Db	181	CATTTTGGGCGCTTAACATTCATCATTAATTCATCTTCGCGGTCCCTTAAGATT	240
Qy	267	CCATCTCTGTGAATCTTAATTCCTCTCAATAACGTTCTCTAATACAGGTCCTTAAGCAA	326
Db	241	CCATCTCTGTGAATCTTAATTCCTCTCAATAACGTTCTCTAATACAGGTCCTTAAGCAA	300
Qy	327	TACCTAATTAAGACATTTTTTAATTTTTTGTACATACATATTTGTCACTCTCAAAATG	386
Db	301	TACCTAATTAAGACATTTTTTAATTTTTTGTACATACATATTTGTCACTCTCAAAATG	360
Qy	387	CATTATACATTTTAAGTTTAACTTAACCGAATATTTAAAGATTAACAAACGATGAAGAAC	446
Db	361	CATTATACATTTTAAGTTTAACTTAACCGAATATTTAAAGATTAACAAACGATGAAGAAC	420
Qy	447	TGTTTGAATAAATCTAATATTAAGAAATCCAGAGAGGTTCTCTAATTTAAGATGATTAT	506
Db	421	TGTTTGAATAAATCTAATATTAAGAAATCCAGAGAGGTTCTCTAATTTAAGATGATTAT	480
Qy	507	TTAAGAGACGCTGTAGAAAACGTAAAAAATCTTTGATTAATTAATATTTAAGGTAGAGT	566
Db	481	TTAAGAGACGCTGTAGAAAACGTAAAAAATCTTTGATTAATTAATATTTAAGGTAGAGT	540
Qy	567	AGCCTTAATGCTTTAATAGATCTTTGGTGTGACCCAGCCTTAATCCGGTTATTTTGGCATT	626
Db	541	AGCCTTAATGCTTTAATAGATCTTTGGTGTGACCCAGCCTTAATCCGGTTATTTTGGCATT	600
Qy	627	GCGCCTCATATTTCACTCCAGAGGCCCAATTTCAAGTTTCAACGAAAGGCCCAAGCC	686
Db	601	GCGCCTCATATTTCACTCCAGAGGCCCAATTTTCAAGTTTCAACGAAAGGCCCAAGCC	660
Qy	687	TGCTTAACCAACAAATTTGTACGCTGTGCGCGGTTTTCAAAAAGAGTGTGAAACCATGTGC	746
Db	661	TGCTTAACCAACAAATTTGTACGCTGTGCGCGGTTTTCAAAAAGAGTGTGAAACCATGTGC	720
Qy	747	ACCACCGACGTAGTAGGCCCTCGGATCTCTCTGATTAAAGTCTTAGCCATATGAGAGCCCA	806
Db	721	ACCACCGACGTAGTAGGCCCTCGGATCTCTCTGATTAAAGTCTTAGCCATATGAGAGCCCA	780
Qy	807	GAACCAACCAATCAAGCGGATGTGTCCCAAGCTTCACTCATGTGGGCGCGGTCATCTCCA	866
Db	781	GAACCAACCAATCAAGCGGATGTGTCCCAAGCTTCACTCATGTGGGCGCGGTCATCTCCA	840
Qy	867	TCCAACAACCTAATCCGTTAATCTTGCCCATCTCTCGAATAAATTTCTCGGCTGTGCGCTCGC	926
Db	841	TCCAACAACCTAATCCGTTAATCTTGCCCATCTCTCGAATAAATTTCTCGGCTGTGCGCTCGC	900
Qy	927	ACCTAATCAAAATACCAATCCCATCCGATCCAGCGCATGTGATCACTGCCAAATCCCCAGAAA	986
Db	901	ACCTAATCAAAATACCAATCCCATCCGATCCAGCGCATGTGATCACTGCCAAATCCCCAGAAA	960
Qy	987	ATCAACAACCTCCCAATTCACAGCGTGCACCAACAATGTGCGCTCTCCGGGCGCAAGACCAAA	1046
Db	961	ATCAACAACCTCCCAATTCACAGCGTGCACCAACAATGTGCGCTCTCCGGGCGCAAGACCAAA	1020
Qy	1047	G 1047	
Db	1021	G 1021	

Db	421	TGTTTGGATTAATTCATATATATATAGAAATCCAGTAGGCTCTCTAAATTTAGATGATTAT	480
QY	507	TTTAGAGGACCGCTGTAGAAAAAGTAAAAATTTCTTTGATTATTTATTTTAGAGGTAGAGT	566
Db	481	TTTAGAGGACCGCTGTAGAAAAAGTAAAAATTTCTTTGATTATTTATTTTAGAGGTAGAGT	540
QY	567	AGGCTTTATGCTTTTATATGATCTTTGGGGGAGCCAGAGCTTATACCGGTTATTTTCGCGATT	626
Db	541	AGGCTTTATGCTTTTATATGATCTTTGGGGGAGCCAGAGCTTATACCGGTTATTTTCGCGATT	600
QY	627	GGCGCTCTCATTTTTCATCTCCAGGCGCCACATTTTTCACGTTTTCACCCGAAGCGCCAGCC	686
Db	601	GGCGCTCTCATTTTTCATCTCCAGGCGCCACATTTTTCACGTTTTCACCCGAAGCGCCAGCC	660
QY	687	TGCTTAAACCAACAATTTGGTACGGTGGCGGGGTTTTCAAAAAGAGTGGAAACCATCTGC	746
Db	661	TGCTTAAACCAACAATTTGGTACGGTGGCGGGGTTTTCAAAAAGAGTGGAAACCATCTGC	720
QY	747	ACCCACCGACATGATGAGGCGCCTCGGATCTCTCCGATTAAAGTCTTAAGCCAAATGAGGAGCCCA	806
Db	721	ACCCACCGACATGATGAGGCGCCTCGGATCTCTCCGATTAAAGTCTTAAGCCAAATGAGGAGCCCA	780
QY	807	GAACCAACCAATCAACGCGGATCGTCCCTCAAGCTTTCACCTCATCGGCGCGCTCCATCTCCA	866
Db	781	GAACCAACCAATCAACGCGGATCGTCCCTCAAGCTTTCACCTCATCGGCGCGCTCCATCTCCA	840
QY	867	TCCAAACACTATTTCCGTTACCTTGGCCCATCTCTCGAAAAAATTTCTGGGCTTCGGCTCCGC	926
Db	841	TCCAAACACTATTTCCGTTACCTTGGCCCATCTCTCGAAAAAATTTCTGGGCTTCGGCTCCGC	900
QY	927	ACCCACATCAAAATATCCCATCCCATCAGACGAGCATCGATCAGTCAGCCAAATCCCCACAGAA	986
Db	901	ACCCACATCAAAATATCCCATCCCATCAGACGAGCATCGATCAGTCAGCCAAATCCCCACAGAA	960
QY	987	ATCAACACCTCCCAATTTCCAGCGTGCACCAACATCGCGCTCTTCGCGCCAGCACCAAA	1046
Db	961	ATCAACACCTCCCAATTTCCAGCGTGCACCAACATCGCGCTCTTCGCGCCAGCACCAAA	1020
QY	1047	G 1047	
Db	1021	G 1021	
RESULT 7			
MZEH3C4			
LOCUS	MZEH3C4	1264 bp	DNA linear PLN 27-APR-1993
DEFINITION	Maize (Zea mays) histone H3 gene (H3C4), complete cds.		
ACCESSION	M13379		
VERSION	M13379.1	GI:168496	
KEYWORDS	histone.		
SOURCE			
ORGANISM	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 1264)		
AUTHORS	Chaubet,N., Phillips,G., Chaboute,M.-E., Ehling,M. and Gigot,C.		
TITLE	Nucleotide sequences of two corn histone H3 genes. Genomic organization of the corn histone H3 and H4 genes		
JOURNAL	Plant Mol. Biol. 6, 253-263 (1986)		
COMMENT	Original source text: Maize DNA, clone H3C4. Draft entry and printed copy of the sequence [1] kindly provided by C.Gigot, 10-OCT-1986.		
FEATURES	Location/Qualifiers		
source	1..1264		
	/organism="Zea mays"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:4577"		
	526..936		
	/note="histone H3"		
	/codon_start=1		
	/protein_id="AAA3473.1"		

/db xref="GI:168497"
/translation="MARTKOTAKSNGKAPKQATKARKSPATGKRRRP
GIVAKREIKIKQSTBELIKLPQKRVRIADPFKIDLFQSSAVAAIDAEAVLV
GIFEDYNLCIAHAKRVTIMPKDIQLARRINGERA"
ORIGIN 54 bp upstream of BglII site.

Query Match 31.7%; Score 496.4; DB 8; Length 1264;
Best Local Similarity 95.9%; Pred. No. 6,7e-96;
Matches 520; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 531 AAAAATCTTGTATTTATTTAGGTAGAGTACCTTATGCTTATAGATCTT 590
DB 2 AAAATTTCTTGTATTTATTTAGGTAGAGTACCTTATGCTTATAGATCTT 61
QY 591 GGTGAGACCAACCTTATACCGGTTATTTGCGATTTGCGCTCTCATTTTCACTCCA-6C 649
DB 62 GGTGAGACCAACCTTATACCGGTTATTTGCGATTTGCGCTCTCATTTTCACTCCAGC 121
QY 650 GCGCCACATTTTACAGTTTACCGAAGCGCCCGCTGCTTAACCAACAATTTGTACG 709
DB 122 GCGCCACATTTTACAGTTTACCGAAGCGCCCGCTGCTTAACCAACAATTTGTACG 181
QY 710 GTGACGCGGTTTCAAAAGTGGAAACCATCTGACCCACGACTAGTAGGCGCTCG 769
DB 182 GTGACGCGGTTTCAAAAGTGGAAACCATCTGACCCACGACTAGTAGGCGCTCG 241
QY 770 GATCTCTCTGATTAGTCTTACGCAATAGAGCCCAAGAACCAACCATCAACGCGATCGT 829
DB 242 GATCTCTCTGATTAGTCTTACGCAATAGAGCCCAAGAACCAACCATCAACGCGATCGT 301
QY 830 CCTTACGCTTCACTATGCGCGCGCTCCATCTCCATCAACCACTTATCCGTACCTT 889
DB 302 CCTTACGCTTCACTATGCGCGCGCTCCATCTCCATCAACCACTTATCCGTACCTT 361
QY 890 GCCCATCTCCGAAAAATCTGCGCTGCGCTCCGACCTACATCAACAATACCATCCA 949
DB 362 GCCCATCTCCGAAAAATCTGCGCTGCGCTCCGACCTACATCAACAATACCATCCA 421
QY 950 TCAAGACGATCGATCACTGCAAAATCCCGCAAAAATCAACACTCCCAATTTCCAGC 1009
DB 422 TCAAGACGATCGATCACTGCAAAATCCCGCAAAAATCAACACTCCCAATTTCCAGC 481
QY 1010 TCGCACCAACTCGCGCTCTCCGCGCCAGACCAACAAGATTGCCGCCACCGCGGTG 1069
DB 482 TCGCACCAACTCGCGCTCTCCGCGCCAGACCAACAAGATTGCCGCCACCGCGGTG 541
QY 1070 AG 1071
DB 542 AG 543

RESULT 8
AY452735 4895 bp DNA circular SYN 19-DEC-2003
LOCUS Reporter vector pACTXN, complete sequence.
DEFINITION AY452735
ACCESSION AY452735
VERSION AY452735.1 GI:39636979
KEYWORDS Reporter vector pACTXN
SOURCE Reporter vector pACTXN
ORGANISM Other sequences; artificial sequences; vectors.
REFERENCE
1 (bases 1 to 4895)
Vickers, C.E., Xue, G.P. and Greshoff, P.M.
A synthetic xylanase as a novel reporter in plants
JOURNAL Plant Cell Rep. 22 (2), 135-140 (2003)
MEDLINE 22867549
PUBMED 12845475
REFERENCE
2 (bases 1 to 4895)
Vickers, C.E.
Direct Submission
TITLE Submitted (29-OCT-2003) ARC Centre for Integrative Legume Research,
JOURNAL The University of Queensland, Room 213, John Hines Building (69),
St. Lucia, QLD 4072, Australia

FEATURES

source

Location/Qualifiers
1..4895
/organism="Reporter vector pACTXN"
/mol_type="other DNA"
/db_xref="taxon:255329"

misc_feature

/note="sequence from cloning vector pBR322"
468..1328
/note="ampicillin resistance protein; bla"

CDS

/codon_start=1
/product="beta-lactamase"
/protein_id="AA029085.1"
/db_xref="GI:39636980"
/translation="NSIQHFRVALTLPFAFLGIPVPAHPELVKVVDAEDQCARVY
ISLDLNSGKILSFPRPERFPMWSTFVKVLCGAVLSRIDAGQQLRILHYSNDLVE
VSPVEKHLLIDQTVRELCSAAITMSDNTAAILATTIGPKELTAFHNGDHVTRL
DWSEPLNBAI PNDERDFTTPVAMAATTLLKLGELTLASRQQLIDMNEADVAGPL
LRSALPAGVFIAIDKSGAGERSRGIIAALGPDKSRIVIVITTSQATMDERNQIA
EIGASLIRKM"
2345..2367
/note="T7 RNA polymerase promoter"
2426..3338
/note="from rice actin gene; Act1"
3339..3792
/note="intron 1 from rice actin gene; Act1"
3800..4513
/gene="sxYna"
/gene="sxYna"
/note="synthetic xylanase"
/codon_start=1
/product="Xylanase"
/protein_id="AA029086.1"
/db_xref="GI:39636981"
/translation="MASNGKFTYNGQNGOHGVNDGFSYEIWLDMYTGNSWTLTSG
ATPKAEWNAAVRNGLIARGLDPSOKKATLDYDGLVATVQTAASGNSRLCV
YGMFQRLANGPLVBYITIEDVMVNPVPAQGRMTTIDAOYKITGMIDTPTINGG
ETFKQYFSVRQQRKTSGHITVSDHFKEWAKQMGIGNLVEALNAGWOSGVADVTL
LDVYTPPKSSPSATSAAPR"
4535..4872
/note="from rbcS gene"
4895

misc_feature

2345..2367
/note="T7 RNA polymerase promoter"

promoter

2426..3338
/note="from rice actin gene; Act1"

intron

3339..3792
/note="intron 1 from rice actin gene; Act1"

gene

CDS

/gene="sxYna"
/gene="sxYna"
/note="synthetic xylanase"
/codon_start=1
/product="Xylanase"
/protein_id="AA029086.1"
/db_xref="GI:39636981"
/translation="MASNGKFTYNGQNGOHGVNDGFSYEIWLDMYTGNSWTLTSG
ATPKAEWNAAVRNGLIARGLDPSOKKATLDYDGLVATVQTAASGNSRLCV
YGMFQRLANGPLVBYITIEDVMVNPVPAQGRMTTIDAOYKITGMIDTPTINGG
ETFKQYFSVRQQRKTSGHITVSDHFKEWAKQMGIGNLVEALNAGWOSGVADVTL
LDVYTPPKSSPSATSAAPR"
4535..4872
/note="from rbcS gene"
4895
misc_feature
/note="SP6 RNA polymerase transcription initiation site"

ORIGIN

Query Match 29.3%; Score 458.2; DB 12; Length 4895;
Best Local Similarity 88.7%; Pred. No. 1.2e-87;
Matches 542; Conservative 0; Mismatches 63; Indels 6; Gaps 4;

QY 958 CATCGATCACTGCGCAATCCCGAGAAATCAACACTCCCAATTTCCAGCTGCCACCA 1017
DB 3195 CAAGAAAGCGCCCCCATCGCACTATATACATACCCCCCTCTCCATCCCCCA 3254
QY 1018 ACTGCGGCTCTCCGCGCAAGACCAAGATTGCCGCCACCGCGGTGAGCTTCC 1077
DB 3255 ACCCTACACACACACACACACACACTCTCCCTCTGCTGCGAGACGACGCTCTC 3314
QY 1078 CCCCCCTCCCTCCGCGCGCGCGGTAACACACCGCCCTCTCTCTTTCTCCGT 1137
DB 3315 CCCCCCTCCCTCCGCGCGCGCGGTAACACACCGCCCTCTCTCTTTCTCCGT 3374
QY 1138 TTTTCTTCTGCTCGTCTGATCTTTGAGCTTGTGTAATTTGGTGGGCGAGAGCGCT 1197
DB 3375 TTTTCTTCTGCTCGTCTGATCTTTGAGCTTGTGTAATTTGGTGGGCGAGAGCGCT 3434
QY 1198 TCGTGGCCAGATCGGTGCGGAGGCGGAGATCGCGGCTGCGCTCCGCGCGG 1257
DB 3435 TCGTGGCCAGATCGGTGCGGAGGCGGAGATCGCGGCTGCGCTCCGCGCGG 3494
QY 1258 AGTCGCGCGGATCTCGCGGGAATGCGGCTCTCGATGTAGATCT--GATCCGCGCTT 1315
DB 3495 AGTCGCGCGGATCTCTCGCGGGAATGCGGCTCTCGATGTAGATGTGCGATCCGCGCTT 3554

OY	1316	TTTGGGGGAGNATGGGGGCTTTAAATT--CGCCATGTAAAACAATCAGAAGAG	1374
Dd	3555	GTTGGGGAGATGATGGGGGTTTTAAATTTCCGCCATGCTAACACAGATCAGGAAGG	3614
OY	1375	GGAAAAAGGCCTATGTTTATATTTTATATTTTCGTGCTGCTGTCAGGCTTGA	1434
Dd	3615	GGAAAAAGGCCTATGTTTATATTTTATATTTTCGTGCT--TGCTAGGCTTAGA	3672
OY	1435	TGTGCTATATCTTTCTTCTTTTGTGGGTGAATTTGAATCCCTCACATTTGTA	1494
Dd	3673	TGTGCTAATCTTTCTTTCTTTCTTTTGT--GGTAAATTTGATCCCTCACATTTGTA	3731
OY	1495	TCGGTAGTTTTCCTTTTCATGATTTGTGACAAATGCAAGCCTGTGCGAGCTTTTGTGA	1554
Dd	3732	TCGGTAGTTTTCCTTTTCATGATTTGTGACAAATGCAAGCCTGTGCGAGCTTTTGTGA	3791
OY	1555	GGTAGACCATG	1565
Dd	3792	GGTAGACCATG	3802

RESULT 9					
LOCUS	A94724	454 bp	DNA	linear	PAT 26-JAN-2000
DEFINITION	Sequence 2 from Patent WO934005.				
ACCESSION	A94724				
VERSION	A94724.1	GI:678989			
KEYWORDS	.				
SOURCE	unidentified				
ORGANISM	unidentified				
REFERENCE	unclassified.				
AUTHORS	1 (bases 1 to 454)				
TITLE	Derose,R. and Freyssiuet,G. MAIZE H3CA PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON,				
JOURNAL	CHIMERIC GENE CONTAINING IT AND TRANSFORMED PLANT Patent: WO 934005-A 2 08-Jul-1993;				
FEATURES	PHONE POULENC AGROCHIMIE (FR) Location/Qualifiers				
source	1..454 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"				
ORIGIN	1..454				
intron					
Query Match	29.0%; Score 454; DB 6; Length 454;				
Best Local Similarity	100.0%; Pred.No.7.6e-87;				
Matches	454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1102 GTAAACACCCCGCCTCTCTCTTTTTCCTGTTTTCCTGTCGTGCAT	1161			
DB	1 GTAACACCCCGCCCCCTCTCTCTTTTTCCTGTCGTGCAT	60			
QY	1162 CTTTGCCCTTGTAAGTTGGGTGGCGAAGCGGCTTCGTGCCAGATCGGTGCGGG	1221			
DB	61 CTTTGCCCTTGGAATTGGGTGGCGAGAAGCGGCTTCGTGCCAGATCGGTGCGGG	120			
QY	1222 AGGGGCGGGATTCGCGCGCTGCAGTCTCCGGCGTAGATCGGCCCGCATCTCTGGGGGA	1281			
DB	121 AGGGGCGGGATTCGCGCGCTGCAGTCTCCGGCGTAGATCGGCCCGCATCTCTGGGGGA	180			
QY	1282 ATGGGGCTCTCGGAGTGAATGTGATCGCGCGTGTGTGGGGGAGATGATGGGGCGTTAA	1341			
DB	161 ATGGGGCTCTCGGAGTGAATGTGATCGCGCGTGTGTGGGGGAGATGATGGGGCGTTAA	240			
QY	1342 AATTTCGCATGCTAAACAAGATCAAGAAAGAGGGAAAAAGGCACTATGTTATATTTT	1401			
DB	241 AATTTCGCATGCTAAACAAGATCAAGAAAGAGGGAAAAAGGCACTATGTTATATTTT	300			
QY	1402 TATATATTTCTGCTGCTGCTGCTGAGGCTTAATATGCTGAATCTTTCTTTCTTTT	1461			
DB	301 TATATATTTCTGCTGCTGCTGCTGAGGCTTAATATGCTGAATCTTTCTTTCTTTT	360			

QY	1662	GTGGGTGAAATTTTAAATCCCTCAGACATGTTCAATCGGTAGTTTCTTTTCATGATTTGT	1521
DB	361	GTGGGTGAAATTTGAAATCCCTCAGACATGTTCAATCGGTAGTTTCTTTTCATGATTTGT	420
QY	1522	GACAAATGCAGCCTCGTGCAGAGCTTTTGTGAG	1555
DB	421	GACAAATGCAGCCTCGTGCAGAGCTTTTGTGAG	454
RESULT	10		
LOCUS	AR559744	454 bp	DNA
DEFINITION	Sequence 2 from patent US 6750378.	linear	PAT 08-OCT-2004
ACCESSION	AR559744		
VERSION	AR559744.1	GI:53969842	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 454)		
TITLE	Derose,R. and Freyessinet,G.		
JOURNAL	Maize H304 promoter combined with the first intron of rice actin,		
FEATURES	chimeric gene comprising it and transformed plant		
Source	Patent: US 6750378-A 2 15-JUN-2004;		
	Location/Qualifiers		
	1..454		
	/organism="unknown"		
	/mol_type="genomic DNA"		

Query Match	29.0%	Score 454	DB 6	Length 454
Best Local Similarity	100.0%	Prod. No. 7.6e-87		
Matches 454	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1102	GTAACCAACCCGCGCCCTCTCCTCTTCTTCTCCGTTTTTTCGTCCTCGATCGAT	1161	
Db	1	GTAACCAACCCGCGCCCTCTCCTCTTCTTCTTCTCCGTTTTTTCGTCCTCGATCGAT	60	
QY	1162	CTTTGGCCTTGGTAGTTTGGGTGGGCGAGAGCGGCTTCGTGCGCAAGTCGATCGGCGGG	1221	
Db	61	CTTTGGCCTTGGTAGTTTGGGTGGGCGAGAGCGGCTTCGTGCGCGCAAGTCGATCGGCGGG	120	
QY	1222	AGGGGCGGGAGTCTGCGCGGCTGGCGCTCTCCGGGCGTGAAGTCGGACCCGGATCCTCGCGGGGA	1281	
Db	121	AGGGGCGGGAGTCTGCGCGGCTGGCGCTCTCCGGGCGTGAAGTCGGACCCGGATCCTCGCGGGGA	180	
QY	1282	ATGGGGGCTCTCGAGTAGTAGATCTGATTCGCGCGTGTGGGGGAGATAGTGGGCGGTTTAA	1341	
Db	181	ATGGGGGCTCTCGAGTAGTAGATCTGATTCGCGCGTGTGGGGGAGATAGTGGGCGGTTTAA	240	
QY	1342	AATTTGCGCAGTCGTAACCAAGATCAGGAAGAAGGGGAAAGGGGCACTAAGGTTATATTTT	1401	
Db	241	AATTTGCGCAGTCGTAACCAAGATCAGGAAGAAGGGGAAAGGGGCACTAAGGTTATATTTT	300	
QY	1402	TATATATTTCTGCTGCTGCTGCTGAGGCTTAGATGTGCTAGATCTTTCCTTCTTCTTTT	1461	
Db	301	TATATATTTCTGCTGCTGCTGCTGAGGCTTAGATGTGCTAGATCTTTCCTTCTTCTTTT	360	
QY	1462	GTGGGTAGAAATTTGAATTCCTCAGCATTTGTTCAATCGTAGTTTTCCTTTCATGATTTGT	1521	
Db	361	GTGGGTAGAAATTTGAATTCCTCAGCATTTGTTCAATCGTAGTTTTCCTTTCATGATTTGT	420	
QY	1522	GACAAATGACAGCCTCGTGGCGGAGCTTTTGTAG	1555	
Db	421	GACAAATGACAGCCTCGTGGCGGAGCTTTTGTAG	454	
RESULT 11				
LOCUS BD128390				
DEFINITION Corn H3C4 promoter bonded to the first intron of rice actin,				
chimeric gene containing this promoter and transgenic plant.				
ACCESSION BD128390				

VERSION	BD128390.1	GI:23223335
KEYWORDS	JP 2002500016-A/2.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 454)	
AUTHORS	Durose,R. and Freysaier,G.	
TITLE	Corn H3C4 promoter bonded to the first intron of rice actin,	
JOURNAL	chimeric gene containing this promoter and transgenic plant Patent: JP 2002500016-A 2 08-JAN-2002;	
COMMENT	AVENTIS CROPS SCIENCE SA OS Unidentified PN JP 2002500016-A/2 PD 08-JAN-2002 JP 2000526660 PF 22-DEC-1998 JP 2000526660 PI RICHARD DUROSE, GEORGES FREYSAIER PC C12N15/09,A01H5/00,C07K14/21,C07K14/415,C07K19/00,C12N5/10, PC C1201/68, PC C12N15/00,C12N5/00 CC Strandedness: Single; CC Topology: linear; CC Corn H3c4 promoter bonded to the first intron of rice actin, CC chimeric gene CC containing this promoter and transgenic plant FH Key FT location/Qualifiers FT source 1..454 /organism='Unidentified'.	
FEATURES	location/Qualifiers source 1..454 /organism="unidentified" /mol_type="Genomic DNA" /db_xref="taxon:32644"	
ORIGIN		
Query Match:	29.0%; Score 454; DB 6; Length 454;	
Best Local Similarity	100.0%; Pred. No. 7.6e-87;	
Matches 454; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1102 GTAACACACCGGCCCTCTCTCTTCTTCGTTTCTTCTTGCTCGATCGAT	1161
Db	1 GTAACACACCGGCCCTCTCTCTTCTTCGTTTCTTCTTGCTCGATCGAT	60
OY	1162 CTGTGGCTGTGTAGTTGGTGGGCGAGACCGGCTTCGTCGCCAGATCGATGGCGGG	1221
Db	61 CTGTGGCTGTGTAGTTGGTGGGCGAGACCGGCTTCGTCGCCAGATCGATGGCGGG	120
OY	1222 AGGGCGGGGATCTCGCGGCTGGCGCTCCGGGCGTAGATCGGCCCGGATCCTCGCGGGGA	1281
Db	121 AGGGCGGGGATCTCGCGGCTGGCGCTCCGGGCGTAGATCGGCCCGGATCCTCGCGGGGA	180
OY	1282 ATGGGGCTCTCGGATGTAGATCTGATTCGCGCGTTGTTGGGGAGAATGATGGAGCGTTTAA	1341
Db	181 ATGGGGCTCTCGGATGTAGATCTGATTCGCGCGTTGTTGGGGAGAATGATGGAGCGTTTAA	240
OY	1342 AATTTCGCATGCTAACAAGATCAGAAAGGGGAAAAGGCACTATGTTTATATTT	1401
Db	241 AATTTCGCATGCTAACAAGATCAGAAAGGGGAAAAGGCACTATGTTTATATTT	300
OY	1402 TATATATTTTCGCTGCTGCTCATGAGGCTTAGATGCTTAATCTTTCTTTCTTTTT	1461
Db	301 TATATATTTTCGCTGCTGCTCATGAGGCTTAGATGCTTAATCTTTCTTTCTTTTT	360
OY	1462 GTGGGTAGATTTGAATCCCTCAGCATTTGTCATCGATGTTTCTTTCAATGATTTGT	1521
Db	361 GTGGGTAGATTTGAATCCCTCAGCATTTGTCATCGATGTTTCTTTCAATGATTTGT	420
OY	1522 GACAAATGACGCTTCGTGCGGAGCTTTTGTAG 1555	
Db	421 GACAAATGACGCTTCGTGCGGAGCTTTTGTAG 454	

150114	LOCUS	I50114		1392 bp	DNA	linear	PAT 07-OCT-1997
	DEFINITION	Sequence 6 from patent US 5641876.					
	ACCESSION	I50114					
	VERSION	I50114.1	GI:2472334				
	KEYWORDS	.					
	SOURCE	Unknown.					
	ORGANISM	Unclonified.					
	REFERENCE	1 (bases 1 to 1392)					
	AUTHORS	Mcelroy,D. and Wu,R.					
	TITLE	Rice actin gene and promoter					
	JOURNAL	Patent: US 5641876-A 6 24-JUN-1997;					
	FEATURES	Location/Qualifiers					
	SOURCE	1..1392					
		/organism="unknown"					
	ORIGIN	/mol_type="unassigned DNA"					
	Query Match	27.4%; Score 428.8; DB 6; Length 1392;					
	Best Local Similarity	84.9% Pred.No. 2.2e-81;					
	Matches 518; Conservative 0; Mismatches 82; Indels 10; Gaps 3;						
OY	958	CATGCGATCACTGGCCAATCCGCCAGAAATCAACACTCCTGCCAATTGCAGCTGCACGA	1017				
DB	775	CAAAGAAAACGTCCCCCATTCGCCACTATAATACATACCCTTCTCTCCATCCCCCA	834				
OY	1018	ACTGCGCGCTCTCCGCGCACAGAACAAGGAATTTGACCGGACCGGCGTGGAAGCTCTC	1077				
DB	835	ACCCTAACACACACACACACACACACACCTCTCCCCTCGCTGCGGAGACGAGACTCTC	894				
OY	1078	CCCCCTCCCCCTCGCGCGCGCGGTAAACACCCCG--CCCTCTCTCTTTTCTTC	1135				
DB	895	CCCCCTCCCCCTCGCGCGCGCGGTAAACACCCCGGTCTCTCTCTTTCTTCTCC	954				
OY	1136	GTTTTTTTTTCGTGCTGGTCTGATCTTTTGACCTTAGTTGGTGGGCGAGACGG	1195				
DB	955	GTTTTTTTTTCGTCTGCTGCTGATCTTTTGACCTTAGTTGGTGGGCGAGAG-GCGG	1013				
OY	1196	CTTCGTGCGCCAGATCGGTGCGGCGGAGCGGGAATCTCGCGCTGCGCTTCCTCCGGAGCG	1255				
DB	1014	CTTCGTGCGCCAGATCGGTGCGGCGGAGCGGGAATCTCGCGCTG-----GTCTC	1066				
OY	1256	TGAGTCCGCCCGGATCTCTCGCGSGGAATGGGGCTCTCGAGATGATCTGATCCCGCTT	1315				
DB	1067	GGCGTGCGGCGCGGATCTCTCGCGSGGAATGGGGCTCTCGAGATGATCTGATCCCGCTT	1126				
OY	1316	GTTGGGGGAGATGATGGGGCGTTAAAAATTTGCGCATGTAAACAATCAGAGAAGGG	1375				
DB	1127	GTTGGGGGAGATGATGGGGCGTTAAAAATTTGCGCATGTAAACAATCAGAGAAGGG	1186				
OY	1376	GAAGAAGGCACTAGTTTATATTTATATTTATTTCTGCTGCTGCTGACGCTTAGAT	1435				
DB	1187	GAAGAAGGCACTAGTTTATATTTATATTTATTTCTGCTGCTGCTGACGCTTAGAT	1246				
OY	1436	GTCGTAGATCTTCTTCTTCTTTTGGGTAGAAATTTGAATCCTCAGCATTTTCAT	1495				
DB	1247	GTCGTAGATCTTCTTCTTCTTTTGGGTAGAAATTTGAATCCTCAGCATTTTCAT	1306				
OY	1496	CGGTAGTTTTTCTTTTCAATGATTTGRACAAATGCACCTCGTGGAGAGCTTTTTGTAG	1555				
DB	1307	CGGTAGTTTTTCTTTTCAATGATTTGRACAAATGCACCTCGTGGAGAGCTTTTTGTAG	1366				
OY	1556	GTAGACCATG 1565					
DB	1367	GTAAGAGATG 1376					
RESULT 13							
LOCUS	I50115		1404 bp	DNA	linear	PAT 07-OCT-1997	
DEFINITION	Sequence 7 from patent US 5641876.						
ACCESSION	I50115						

VERSION	150115.1	GI:2472335
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 1404)	
TITLE	McElroy,D. and Wu,R.	
JOURNAL	Rice actin gene and promoter	
FEATURES	Patent: US 5641876-A 7 24-UN-1997;	
source	Location/Qualifiers	
	1..1404	
	/organism="unknown"	
ORIGIN	/mol_type="unassigned DNA"	
Query Match	27.4%;	Score 428.8; DB 6;
Best Local Similarity	84.9%;	Pred.No. 2.2e-81;
Matches	518; Conservative	0; Mismatches 82; Indels 10; Gaps 3;
QY	958	CATGCAATCATCTGCCAAATTCCTCCCAAGAAATACACACTCTCCCAATTCACAGCTGCCACCA 1017
DB	785	CAAAAGAAAGCGCCCCCATCGCACATATATACATACCCCCCTCTCCATCCCCCA 844
QY	1018	ACTGCGCGCTCCGCGCGCAAGACCAAGAAATTCGCGGACACCGCGAGTGGAGTCTCTC 1077
DB	845	ACCTACACACACACACACACACACACTCTCTCCCTCTGCTGCGGACGAGAGACTCTTC 904
QY	1078	CCCCCTCCCTCCGCGCGCGCGGTAACACCCCGC--CCCTCTCTCTTTTCTTC 1135
DB	905	CCCCCTCCCTCCGCGCGCGCGGTAACACCCCGCGTCCCTCTCTTTCTTC 964
QY	1136	GTTTCTTTTCTGCTCGCTCCATCTTTGGCTTGGTAGTTTGGGTGGCGAGAGCG 1195
DB	965	GTTTTTTTCTCCGCTCTGCTCCATCTTTGGCTTGGTAGTTTGGGGCGAGAG-GCGG 10233
QY	1196	CTTGTCGCCAGATCGAGTGGCGGAGAGGCGGAGATCTCGCGGCTGCGTCCGCGCG 1255
DB	1024	CTTGTCGCCAGATCGAGTGGCGGAGAGGCGGAGATCTCGCGCTG9-----GTCTC 1076
QY	1256	TGAGTCGCGCCGCGATCTCGCGGAGATGGGGCTCTCGAGTGTAGATCTGATCCGCGTT 1315
DB	1077	GCGTGGCGCGGATCTCGCGGAGATGGGGCTCTCGAGTGTAGATCTGATCCGCGTT 1136
QY	1316	GTTGGGGAGATGATGGGGCGTTTAAATTCGCATCTTAAACAATTCAGAGAGGG 1375
DB	1137	GTTGGGGAGATGATGGGGCGTTTAAATTCGCATCTTAAACAATTCAGAGAGGG 1196
QY	1376	GAAAGGGACATAGCTTATATTTTATATTTCTGCTGCTGTCGAGGCTTGAT 1435
DB	1197	GAAAGGGACATAGCTTATATTTTATATTTCTGCTGCTGTCGAGGCTTGAT 1256
QY	1436	GTCATGATCTTCTCTCTCTTTTGTGGTAGATTTGAAATCCCTCAGATTTTCAT 1495
DB	1257	GTCATGATCTTCTCTCTCTTTTGTGGTAGATTTGAAATCCCTCAGATTTTCAT 1316
QY	1496	CGGATGTTTTCTTTTCAATGATTTGTACAAATGACGCTCGTGGAGCTTTTGTAG 1555
DB	1317	CGGATGTTTTCTTTTCAATGATTTGTACAAATGACGCTCGTGGAGCTTTTGTAG 1376
QY	1556	GTAGACATG 1565
DB	1377	GTAGAAGATG 1386
RESULT 14		
LOCUS	150113	2199 bp DNA linear PART 07-OCT-1997
DEFINITION	Sequence 5 from patent US 5641876.	
ACCESSION	150113	
VERSION	150113.1	GI:2472333
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	

REFERENCE	1 (bases 1 to 2199)
AUTHORS	McElroy, D. and Wu, R.
TITLE	Rice actin gene and promoter
JOURNAL	Patent: US 5641876-A 5 24-JUN-1997;
FEATURES	Location/Qualifiers
source	1..2199
ORIGIN	/organism="unknown" /mol_type="unassigned DNA"
Query Match	27.4%; Score 428.8; DB 6; Length 2199;
Best Local Similarity	84.9%; Pred. No. 2.3e-81;
Matches 518; Conservative 0; Mismatches 82; Indels 10; Gaps 3;	
Qy	958 CATGCATCACTGCCAAATCCCCAGAAATCAACACTCTCCAAATTCACGCTGCCACCA 1017
Db	1582 CAAAGAAACGCCCCCATCGCCACTATATACATACCCCCCTCTCTCCATCCCCCA 1641
Qy	1018 ACTGCGCTCTTCGCGCGCAAGACCAAGAAATGAGCCGACACGGGAGGACTCTC 1077
Db	1642 ACCCTACACACACACACACACACTCTCTCCCCCTGCTGCGCGACAGACACTCTC 1701
Qy	1078 CCCCCCTCCCCCTCGCGCGCGCGCGTAAACACCCCGC--CCCTCTCTCTTTCTTCTCC 1135
Db	1702 CCCCCCTCCCCCTCGCGCGCGCGGTAACACCCCGGCTCCCTCTCTTTCTTCTCC 1761
Qy	1136 GTTTTTTTTTTGCTCGCTCGCTCGATCTTTGGCTTGGTAGTTGGGTGGCGAGACCG 1195
Db	1762 GTTTTTTTTTTCCCTCTGCTCTCGATCTTTGGCCTTGGTAGTTGGGAGGCGAAG-CCGG 1820
Qy	1196 CTTGCGCGCCAGATCGGTGCGCGGAGGCGGAGATCTCGCGGCTGGCGCTCCGAGCG 1255
Db	1821 CTTCGTGCGCCAGATCGGTGCGCGGAGGCGGAGATCTCGCGGCTGG-----GTCTC 1873
Qy	1256 TGAAGTCGCGCCGGAATCTCGCGGGAATGGGGCTCTCGAGTAGTAGATCTGATCCGCGTT 1315
Db	1874 GCGGTGCGCGCGGATCTCTCGCGGGAATGGGGCTCTCGAGTAGTAGATCTGATCCGCGTT 1933
Qy	1316 GTTGGGGAGATGATGGGGCGTTTAAATTTGCGCATGCTTAAACAAGATCAGAAAGGG 1375
Db	1934 GTTGGGGAGATGATGGGGCGTTTAAATTTGCGCATGCTTAAACAAGATCAGAAAGGG 1993
Qy	1376 GAAAAGGCACTAATGTTAATTTTAATTTTCTGCTGCTGCTGCTGCAAGCTTATGAT 1435
Db	1994 GAAAAGGCACTAATGTTAATTTTAATTTTCTGCTGCTGCTGCTGCAAGCTTATGAT 2053
Qy	1436 GAGCTAGATCTTCTCTTCTCTTTTGGGGTAGAATTTGAATCCCTCAGCATTTTCAT 1495
Db	2054 GTGCTAGATCTTCTCTTCTCTTTTGGGGTAGAATTTGAATCCCTCAGCATTTTCAT 2113
Qy	1496 CGGTAGTTTTCTTTCAATGATTTGTGCAAAATCAAGCTGTCGAGACTTTTGTAG 1555
Db	2114 CGGTAGTTTTCTTTCAATGATTTGTGCAAAATCAAGCTGTCGAGACTTTTGTAG 2173
Qy	1556 GTAGACCATG 1565
Db	2174 GTAGAAAGATG 2183
RESULT 15	
LOCUS	150112 5643 bp DNA linear PAT 07-OCT-1997
DEFINITION	Sequence 4 from patent US 5641876.
ACCESSION	150112
VERSION	150112.1 GI:2472332
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 5643)
AUTHORS	McElroy, D. and Wu, R.
TITLE	Rice actin gene and promoter

JOURNAL Patent: US 5641876-A 4 24-JUN-1997;
FEATURES Location/Qualifiers
SOURCE 1..5643
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 27.4%; Score 428.8; DB 6; Length 5643;

Best Local Similarity 84.9%; Pred. No. 2.6e-81;
Matches 518; Conservative 0; Mismatches 82; Indels 10; Gaps 3;

```
QY 958 CATGCATCACTGCGCAATCCCGCAAAATCAACACCTCCCAATTCACGCTGCACCA 1017
   |||||
Db 1585 CAAAGAAACGCCCCCTCGCACTATATACATACCCCCCTCTCCATCCCCCA 1644
   |||||
QY 1018 ACTGCGCTCTCGCGCAAGCAACAAAGAAATGGCCGACCGCGATGAGCTCTC 1077
   |||||
Db 1645 ACCCTACACACCAACCAACCACTCTCCCTCGCTGCGAGAGAGAGCTCTC 1704
   |||||
QY 1078 CCCCCTCCCCCTCGCGCGCGCGGTAAACACCCCGC--CCCTCTCTCTTTCTTCC 1135
   |||||
Db 1705 CCCCCTCCCCCTCGCGCGCGCGGTAAACACCCCGCTCTCTCTTTCTTCC 1764
   |||||
QY 1136 GTTTTCTTTTCTGCTCGATCTGATCTTTGGCTTGTGGGTGGGCGAGAGCG 1195
   |||||
Db 1765 GTTTTCTTTTCTGCTCGATCTGATCTTTGGCTTGTGGGTGGGCGAGAG-CCGG 1823
   |||||
QY 1196 CTTCGCGCCAGATCGGATCGCGGAGCGGAGATCTCGCGCTCTCCGCGCG 1255
   |||||
Db 1824 CTTCGCGCCAGATCGGATCGGAGCGGAGATCTCGCGCTG-----GTCTC 1876
   |||||
QY 1256 TGAATCGCCCGGATCTCGCGGAGAAATGGGCTCTCGAATGATCTGATCCGCGTT 1315
   |||||
Db 1877 GCGCTGCGCGCGGATCTCGCGGAGAAATGGGCTCTCGAATGATCTGATCCGCGTT 1936
   |||||
QY 1316 GTTGGGGGAGATGATGGGGGCTTAAATTCGCAATCTAAACAAGATCAGGAAGGG 1375
   |||||
Db 1937 GTTGGGGGAGATGATGGGGGCTTAAATTCGCAATCTAAACAAGATCAGGAAGGG 1996
   |||||
QY 1376 GAAAGGGCACTATGTTTATATTTTATATTTCTGCTGCTGCTCAGGCTTAGAT 1435
   |||||
Db 1997 GAAAGGGCACTATGTTTATATTTTATATTTCTGCTGCTGCTCAGGCTTAGAT 2056
   |||||
QY 1436 GTGCTAGATCTTTCTTCTTTTGGGTAGAAATTTGAATCCTCAGCATTTTCAT 1495
   |||||
Db 2057 GTGCTAGATCTTTCTTCTTTTGGGTAGAAATTTGAATCCTCAGCATTTTCAT 2116
   |||||
QY 1496 CGGATGTTTCTTTTATATTTTGAACAATGACAGCTTGGAGGCTTTTGTAG 1555
   |||||
Db 2117 CGGATGTTTCTTTTATATTTTGAACAATGACAGCTTGGAGGCTTTTGTAG 2176
   |||||
QY 1556 GTAGACCATG 1565
   |||||
Db 2177 GTAGAACATG 2186
   |||||
```

Search completed: September 12, 2005, 02:27:07
Job time : 4921.01 secs

THIS PAGE BLANK (USPTO)

(AAZ91038). The chimeric regulatory region is useful for the expression of heterologous genes that confer resistance to certain herbicides, or that have novel agronomical properties in monocotyledons. In particular, the chimeric 5' regulatory gene is linked to an enzyme that confers resistance to a specific herbicide. This is useful for controlling weeds in fields of plants/grains that have been transformed with the chimeric gene. The herbicide can be applied to the field without affecting the plant/grain. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 1565 BP; 366 A; 415 C; 297 G; 487 T; 0 U; 0 Other;

Query Match 100.0%; Score 1565; DB 2; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GAATTCCTGACAGTCCGATCCCTTATGTGCACCAATTTCTGTATGCAATTCAT 60
DB 1 GAATTCCTGACAGTCCGATCCCTTATGTGCACCAATTTCTGTATGCAATTCAT 60
QY 61 TTAATTGAATAGCAACTTTCTATTACTCTTACTAATCATTAATCTGGTTTAAAT 120
DB 61 TTAATTGAATAGCAACTTTCTATTACTCTTACTAATCATTAATCTGGTTTAAAT 120
QY 121 TCAGTCTCAACATTCATTCCTCAAGTATAGTGAAGTCAAAATTTACTATTTAT 180
DB 121 TCAGTCTCAACATTCATTCCTCAAGTATAGTGAAGTCAAAATTTACTATTTAT 180
QY 181 TTCTTCAATTTTTTTTCTTATACATATTTGGGCTTACATTCATCTATATCCA 240
DB 181 TTCTTCAATTTTTTTTCTTATACATATTTGGGCTTACATTCATCTATATCCA 240
QY 241 TCCCTTCCGGTGCCTCTAATAAAGTTCATCTCTGATCTPATTCCTCCAAATACG 300
DB 241 TCCCTTCCGGTGCCTCTAATAAAGTTCATCTCTGATCTPATTCCTCCAAATACG 300
QY 301 TCTCTAATCAGGTCCTCTATAGCAATACCTATATTAGAGACATTTTATTTTGTAC 360
DB 301 TCTCTAATCAGGTCCTCTATAGCAATACCTATATTAGAGACATTTTATTTTGTAC 360
QY 361 ATTCATATTTGTATCTCTCAAAATGATATATATTTAGTTTATCTAAACCATAT 420
DB 361 ATTCATATTTGTATCTCTCAAAATGATATATATTTAGTTTATCTAAACCATAT 420
QY 421 TTAAGATTCGAACGAGTGAAGACGTTAGTAAATCTATATATAGAGATCAGT 480
DB 421 TTAAGATTCGAACGAGTGAAGACGTTAGTAAATCTATATATAGAGATCAGT 480
QY 481 AGCGTTCTTAAATTTAGATGATTTATTAGAGACGCTGTAGAAAAAGTAAAAATTC 540
DB 481 AGCGTTCTTAAATTTAGATGATTTATTAGAGACGCTGTAGAAAAAGTAAAAATTC 540
QY 541 TTGATTTATTTATTTAGGATAGATAGCTTTATATGCTTTATATGATTTGGTGACCA 600
DB 541 TTGATTTATTTATTTAGGATAGATAGCTTTATATGCTTTATATGATTTGGTGACCA 600
QY 601 GCGTTATACCGGTTATTTGCGATTCGCGCTCATTTTCATCCAGCCGCCACATTT 660
DB 601 GCGTTATACCGGTTATTTGCGATTCGCGCTCATTTTCATCCAGCCGCCACATTT 660
QY 661 TCACGTTTTCAACGAGCGCCAGCTGCTTAAACCAAAATTTGTACGCTGGCGGTT 720
DB 661 TCACGTTTTCAACGAGCGCCAGCTGCTTAAACCAAAATTTGTACGCTGGCGGTT 720
QY 721 TTCAAAAGAGTGGAAACATCTGCAACCGACTAGTAGGCGCTCGATCTCCCTG 780
DB 721 TTCAAAAGAGTGGAAACATCTGCAACCGACTAGTAGGCGCTCGATCTCCCTG 780
QY 781 ATTAAGCTTAGGCAATAGAGCCAGAACCAACCAACCAACGCGATGCTCCCTACGCTTC 840
DB 781 ATTAAGCTTAGGCAATAGAGCCAGAACCAACCAACCAACGCGATGCTCCCTACGCTTC 840
QY 841 CACCTCATCGGCGCGCTCATCTCAACCAACCTATTCGTTACCTTGCATCTCC 900
DB 841 CACCTCATCGGCGCGCTCATCTCAACCAACCTATTCGTTACCTTGCATCTCC 900
```

```
DB 841 CACCTCATCGGCGCGCTCATCTCAACCAACCTATTCGTTACCTTGCATCTCC 900
QY 901 GAAAAAATTTCTGGCTGGGCTCGGACCTACTACAAATACCATTCCATCAGAGCAT 960
DB 901 GAAAAAATTTCTGGCTGGGCTCGGACCTACTACAAATACCATTCCATCAGAGCAT 960
QY 961 CGCATCTACTGCAAAATCCCGCAAGAAATCAACACCTCCCAATTCACGCTGCACCACT 1020
DB 961 CGCATCTACTGCAAAATCCCGCAAGAAATCAACACCTCCCAATTCACGCTGCACCACT 1020
QY 1021 CGCGCTCTCGGCGCGCAAGCAACAAAGAAATTTGGCGCACCGCGGTGAGCTCTCCCC 1080
DB 1021 CGCGCTCTCGGCGCGCAAGCAACAAAGAAATTTGGCGCACCGCGGTGAGCTCTCCCC 1080
QY 1081 CCGCCCGCTCGGCGCGCGGTTAACCAACCCCGCTCTCTCTTTCTTTCTCGGTTT 1140
DB 1081 CCGCCCGCTCGGCGCGCGGTTAACCAACCCCGCTCTCTCTTTCTTTCTCGGTTT 1140
QY 1141 TTTTTCGCTCGGCTCGATCTTTTGGCTTGGTGGTGGGCGAGAGCGGCTTCG 1200
DB 1141 TTTTTCGCTCGGCTCGATCTTTTGGCTTGGTGGTGGGCGAGAGCGGCTTCG 1200
QY 1201 TCGCCCAATCGGTCGCGGAGGCGGCGGATCTCGCGCTGCGCTTCGCGGCGTGAAT 1260
DB 1201 TCGCCCAATCGGTCGCGGAGGCGGCGGATCTCGCGCTGCGCTTCGCGGCGTGAAT 1260
QY 1261 CGGCGCGATCTCGCGGCGGAAATGGGCGCTCGGATGATCTGATCGCGCGGCTTGG 1320
DB 1261 CGGCGCGATCTCGCGGCGGAAATGGGCGCTCGGATGATCTGATCGCGCGGCTTGG 1320
QY 1321 GGGAGATGATGGGCGGTTTAAATTTTCGCATGCTTAAACAAATCAGGAAGAGGAGAAA 1380
DB 1321 GGGAGATGATGGGCGGTTTAAATTTTCGCATGCTTAAACAAATCAGGAAGAGGAGAAA 1380
QY 1381 GGGACATATGTTTATTTTATTTATTTTCTGCTGCTGCTGTGAGCTTATGATGTCT 1440
DB 1381 GGGACATATGTTTATTTTATTTTATTTTCTGCTGCTGCTGTGAGCTTATGATGTCT 1440
QY 1441 AGATCTTCTCTCTCTTTTGGGATGAATTTGAATCCCTCAGATTTGTCATCGGTA 1500
DB 1441 AGATCTTCTCTCTCTTTTGGGATGAATTTGAATCCCTCAGATTTGTCATCGGTA 1500
QY 1501 GTTTTCTTTTCAATATTTGTGACAAATGACCTCGTGGCGAGCTTTTGTAGGTAGA 1560
DB 1501 GTTTTCTTTTCAATATTTGTGACAAATGACCTCGTGGCGAGCTTTTGTAGGTAGA 1560
QY 1561 CCATG 1565
DB 1561 CCATG 1565
```

RESULT 2
AAZ91037
ID AAZ91037 standard; DNA; 1021 BP.
XX
XX AAZ91037;
XX
XX 06-JUN-2000 (first entry)
XX
XX Maize histone H3C4 promoter region.
XX DE
XX Regulatory element; monocotyledonous vegetable plant cell; maize;
XX histone H3C4; promoter; rice actin gene intron; chimeric; ss;
XX herbicide resistance.
XX
XX Zea mays.
XX OS
XX PN FR2772787-A1.
XX XX
XX 25-JUN-1999.
XX PD
XX 24-DEC-1997; 97PR-00016726.
XX PF
XX

PR 24-DEC-1997; 97FR-00016726.
 XX (RHON) RHONE-POULENC AGROCHIMIE.
 XX Derose R. Freyssinet G;
 XX WPI; 1999-397352/34.
 DR
 XX
 PT 5' chimeric regulatory region comprising maize histone H3C4 promoter and
 PT rice actin gene first intron.
 XX
 PS Claim 3; Page 13; 24pp; French.
 XX
 CC The invention relates to a DNA sequence (AA291039) comprising a 5'
 CC regulatory element for the expression of a heterologous gene in a
 CC monocotyledonous vegetable plant cell. The DNA comprises: (a) a
 CC functional fragment of the maize histone H3C4 promoter sequence (this
 CC sequence); and (b) a functional fragment of the first intron of the rice
 CC actin gene (AA291038). The chimeric regulatory region is useful for the
 CC expression of heterologous genes that confer resistance to certain
 CC herbicides, or that have novel agronomical properties in monocotyledons.
 CC In particular, the chimeric 5' regulatory gene is linked to an enzyme
 CC that confers resistance to a specific herbicide. This is useful for
 CC controlling weeds in fields of plants/grains that have been transformed
 CC with the chimeric gene. The herbicide can be applied to the field without
 CC affecting the plant/grain
 CC
 XX Sequence 1021 BP; 283 A; 275 C; 140 G; 323 T; 0 U; 0 Other;
 XX
 SQ
 Query Match 65.2%; Score 1021; DB 2; Length 1021;
 Best Local Similarity 100.0%; Pred. No. 1.1e-232;
 Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 627 GGCGCTCTGATTTTCACTCCAGGCGCCCAATTTTCACGTTTTCACGGAAGCGCCAGCC 686
 DB 601 GGCGCTCTGATTTTCACTCCAGGCGCCCAATTTTTCACGTTTTCACGGAAGCGCCAGCC 660
 QY 687 TGGCTAACCAACAATTTGGTACGGTGGCGCGGTTTTCAAAGAAAGTCCGAAACCATCTGC 746
 DB 661 TGGCTAACCAACAATTTGGTACGGTGGCGCGGTTTTCAAAGAAAGTCCGAAACCATCTGC 720
 QY 747 ACCCAGCGACTAGTAGGCGCTCGGATCTCTCGATTAACTGCTTACGCAATAGAGCCCA 806
 DB 721 ACCCAGCGACTAGTAGGCGCTCGGATCTCTCGATTAACTGCTTACGCAATAGAGCCCA 780
 QY 807 GAACCAACCATCAAGGAGATCGTCCCTACGCTTCACTATGAGCGCGCTCCATCTCCA 866
 DB 781 GAACCAACCATCAAGGAGATCGTCCCTACGCTTCACTATGAGCGCGCTCCATCTCCA 840
 QY 867 TCCCAACCATATTCCTTACCTTCCCATCTCCGAAAAATTCGCTCGCTCGC 926
 DB 841 TCCCAACCATATTCCTTACCTTCCCATCTCCGAAAAATTCGCTCGCTCGC 900
 QY 927 ACCTACTCAAAATACCATCCATCCATCAAGCAAGCATGCGATCTGCAAAATCCCGAGAA 986
 DB 901 ACCTACTCAAAATACCATCCATCCATCAAGCAAGCATGCGATCTGCAAAATCCCGAGAA 960
 QY 987 ATCAACACTCCCAATTCAGCGTGGCAACCACTGCGCGTCCGCGGCAAGCAGCAAA 1046
 DB 961 ATCAACACTCCCAATTCAGCGTGGCAACCACTGCGCGTCCGCGGCAAGCAGCAAA 1020
 QY 1047 G 1047
 DB 1021 G 1021

RESULT 3
 AA291038
 ID AA291038 standard; DNA; 454 BP.
 XX
 AC AA291038;
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Rice actin gene intron 1 sequence.
 XX
 KW Regulatory element; monocotyledonous vegetable plant cell; maize;
 KW histone H3C4; promoter; rice actin gene intron; chimeric; ss;
 KW herbicide resistance.
 XX
 OS Oryza sativa.
 XX
 PN FR272787-A1.
 XX
 PD 25-JUN-1999.
 XX
 PF 24-DEC-1997; 97FR-00016726.
 XX
 PR 24-DEC-1997; 97FR-00016726.
 XX
 XX (RHON) RHONE-POULENC AGROCHIMIE.
 XX PI Derose R. Freyssinet G;
 XX WPI; 1999-397352/34.
 DR
 XX
 PT 5' chimeric regulatory region comprising maize histone H3C4 promoter and
 PT rice actin gene first intron.
 XX
 PS Claim 5; Page 14; 24pp; French.
 XX
 CC The invention relates to a DNA sequence (AA291039) comprising a 5'
 CC regulatory element for the expression of a heterologous gene in a
 CC monocotyledonous vegetable plant cell. The DNA comprises: (a) a
 CC functional fragment of the maize histone H3C4 promoter sequence
 CC (AA291037); and (b) a functional fragment of the first intron of the rice

CC	actin gene (this sequence). The chimeric regulatory region is useful for
CC	the expression of heterologous genes that confer resistance to certain
CC	herbicides, or that have novel agronomical properties in monocotyledons.
CC	In particular, the chimeric 5' regulatory gene is linked to an enzyme
CC	that confers resistance to a specific herbicide. This is useful for
CC	controlling weeds in fields of plants/grains that have been transformed
CC	with the chimeric gene. The herbicide can be applied to the field without
CC	affecting the plant/grain
XX	
SQ	Sequence 454 BP; 71 A; 100 C; 133 G; 150 T; 0 U; 0 Other;
	Query Match 29.0%; Score 454; DB 2; Length 454;
	Best Local Similarity 100.0%; Pred. No. 7.3e-96;
	Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1102 GTAACCAACCGGCCCTCTCCCTCTTTCCTCCTGTTTCTTGCTGCATCGATC 1161
Dd	1 GTAACCAACCGGCCCTCTCCCTCTTTCCTCCTGTTTCTTGCTGCATCGATC 60
OY	1162 CTGTGGCCTTGTAAGTTGGGTGGGCGAAGACGAGCTTGTGTGCGCCAGATCGGTGCGGG 1221
Dd	61 CTGTGGCCTTGTAAGTTGGGTGGGCGAAGACGAGCTTGTGTGCGCCAGATCGGTGCGGG 120
OY	1222 AGGGGCGGGAACTCGCGGCTGGCGCTCCCGGGCGTAGTGTGCGCCCGGATCCTCGCGGGGA 1281
Dd	121 AGGGGCGGGAACTCGCGGCTGGCGCTCCCGGGCGTAGTGTGCGCCCGGATCCTCGCGGGGA 180
OY	1282 ATGGGGCTCTCGGAGTGTAGATCTGATCCGCGCTTGTGGGGAGATGATGGGGCGTTTAA 1341
Dd	181 ATGGGGCTCTCGGAGTGTAGATCTGATCCGCGCTTGTGGGGAGATGATGGGGCGTTTAA 240
OY	1342 AATTTCGCGCATGTCAAACAAGATCAGAAGAGGGGAAAAAGGCGACTATGTGTTATATTTT 1401
Dd	241 AATTTCGCGCATGTCAAACAAGATCAGAAGAGGGGAAAAAGGCGACTATGTGTTATATTTT 300
OY	1402 TATAATTTTCGTGCTGCTGCTGTGACGGCTTAGATGTGTAATCTTCTTTCTTTT 1461
Dd	301 TATAATTTTCGTGCTGCTGCTGTGACGGCTTAGATGTGTAATCTTCTTTCTTTT 360
OY	1462 GTGGGTGAATTTGAAATCCCTCAGCATTTGTCATCGTAGTTTTTCTTTTCATGATTTGT 1521
Dd	361 GTGGGTGAATTTGAAATCCCTCAGCATTTGTCATCGTAGTTTTTCTTTTCATGATTTGT 420
OY	1522 GACAAATGACAGCTCTGTGCGGAGCTTTTGTAG 1555
Dd	421 GACAAATGACAGCTCTGTGCGGAGCTTTTGTAG 454
RESULT 4	
ID	ADP73931
ADP73931	standard; DNA; 13680 BP.
XX	ADP73931;
AC	
DT	09-SEP-2004 (first entry)
XX	
DE	Plasmid pDAB8505, SEQ ID NO:85, encoding mAb HX8 (both chains).
XX	
KW	Transgenic plant; immunoglobulin production; recombinant production;
KW	glycosylation; glucose; glycan; virulence; immunotherapy; maize;
KW	gamma-zeta promoter; rice; actin promoter;
KW	phosphonochitin acyltransferase; PAR; mouse; leader sequence;
KW	herpes simplex virus; HSV1; HSV2; human; monoclonal antibody HX8; IGA;
KW	heavy chain; light chain; codon optimised; plasmid; pDAB8505; cyclic;
KW	circular; ds.
XX	
Zea mays.	
Mus sp.	
Homo sapiens.	
Oryza sativa.	
Chimeric.	
Synthetic.	
Undetected.	

XX		Location/Qualifiers
FH	Key	424..1589
FT	misc_feature	/tag= a
FT		/label= SAR
FT		/note= "Scaffold attachment region. Also referred to as
FT		MAR (matrix association region)"
FT	promoter	1673..3175
FT		/tag= b
FT		/note= "Maize gamma-zein promoter"
FT	CDS	3178..4671
FT		/tag= d
FT		/product= "Heavy chain of human anti-HSV1/HSV2 monoclonal
FT		IgA antibody HX8 (with mouse leader sequence)"
FT	sig_peptide	3178..3234
FT		/tag= c
FT		/note= "Mouse leader sequence"
FT	mat_peptide	3235..4668
FT		/tag= e
FT		/product= "Mature HX8 heavy chain"
FT	3'UTR	4678..5045
FT		/tag= f
FT		/note= "Maize peris 3'UTR"
FT	promoter	5157..6659
FT		/tag= g
FT		/note= "Maize gamma-zein promoter"
FT	CDS	6662..7363
FT		/tag= i
FT		/product= "Heavy chain of human anti-HSV1/HSV2 monoclonal
FT		IgA antibody HX8 (with mouse leader sequence)"
FT	sig_peptide	6662..6718
FT		/tag= h
FT		/note= "Mouse leader sequence"
FT	mat_peptide	6719..7360
FT		/tag= j
FT		/product= "Mature HX8 heavy chain"
FT	3'UTR	7370..7737
FT		/tag= k
FT		/note= "Maize peris 3'UTR"
FT	promoter	7889..9258
FT		/tag= l
FT		/note= "rice actin promoter/intron"
FT	CDS	9261..9815
FT		/tag= m
FT		/product= "Phosphinothricin acyltransferase (PAT)"
FT		/note= "The PAT coding region is given in the
FT		specification as positions 9260-9820"
FT	3'UTR	9831..10162
FT		/tag= n
FT		/note= "Maize lipase 3'UTR"
FT	misc_feature	10229..11394
FT		/tag= o
FT		/label= SAR
FT		/note= "Scaffold attachment region. Also referred to as
FT		MAR (matrix association region)"
PV		WO2004050838-A2.
PD		17-JUN-2004.
PF		28-NOV-2003; 2003WO-US037905.
PR		27-NOV-2002; 2002US-0429385P.
PA	(DOMC) DOM CHEM CO.	
PA	(DOMC) DOM AGRSCIENCES LLC.	
PA	(EPIC-) EPICYTE PHARM INC.	
PI	Bridge K, Glancy T, Hein MB, Hiatt AC, Karnoup AL, Anderson WHK,	
PI	Paredy D, Pecolino J, Rubin-Wilson B, Taylor D, Roberts JL,	
WI	WI; 2004-461111/43.	
P-P	P-PSDB; ADP73848, ADP73856.	

XX Novel plant-produced immunoglobulin having glycopeptide or glycan profile
PT with reduced fucosylation, useful for creating herpes simplex virus
PT infection.
PS Claim 69; SEQ ID NO 85; 212pp; English.
XX
CC The invention relates to the production of immunoglobulins in plants,
CC wherein at least a portion of the glycans attached to the immunoglobulins
CC lack fucose. The immunoglobulins produced can be of any class (i.e., IgG,
CC IgA, IgM, IgD or IgE) and is especially an anti-herpes simplex virus
CC (HSV) antibody or an anti-alphaHerpes3, alphaHerpes5 dual integrin
CC antibody. The invention also relates to constructs, plasmids and vectors
CC for producing the immunoglobulins; transformed plant cells, calli, plant
CC tissues and whole plants for producing the immunoglobulins; methods for
CC producing the immunoglobulins, the immunoglobulins thus produced; and the
CC use of such immunoglobulins. The immunoglobulins of the invention may be
CC used to treat HSV infection or tumour angiogenesis. The invention
CC provides the advantages of antibody production in plants, such as large
CC scale production, reduced costs, and elimination of pathogenic
CC contaminants such as viruses and prions, with a simplified (i.e., non-
CC plant-specific) glycosylation profile which reduces the risk that the
CC immunoglobulin may not be functional in animals. The present sequence
CC represents the plasmid pDB8505, which contains codon optimised DNA
CC sequences encoding the heavy and light chains of the human anti-HSV1/HSV2
CC monoclonal IgA antibody HX8 each of which are fused to mouse leader
CC sequences. Both heavy and light chain fusion genes are under the control
CC of maize endosperm-specific gamma-zein promoters. The plasmid also
CC contains a phosphothricin acyltransferase (PAT) gene under the control
CC of a rice actin promoter.
XX
SQ Sequence 13680 BP; 3886 A; 3069 C; 2934 G; 3788 T; 0 U; 3 Other;
Query Match 28.5%; Score 445.6; DB 12; Length 13680;
Best Local Similarity 88.4%; Pred. No. 2.7e-95;
Matches 543; Conservative 0; Mismatches 59; Indels 12; Gaps 5;
QY 958 CATGCATCACTGCGCAATCCCGCAAGAAATCAACACCTCCGATTCACGCTGCACCA 1017
DB CAAAGAAACGCCCGCCATCCGCACTATATACATACCCCGCTCCCTCCATCCCGCCA 8715
QY 1018 ACTGCGCGTCTCCGCGCCCAAGCAACAAAGAAATGCGCGCGCGGTGAGACTCCTC 1077
DB ACCCTACACACACACACACACACAC---TCTCTCCCGCTCGTGCAGACAGCGCTC 8771
QY 1078 CCCCCTCCCTCCGCGCGCGCGCGTAACACACCCGCGCTCTCTTTCTTTCTCCGT 1137
DB CCCCCTCCCTCCGCGCGCGCGCGTAACACACCCGCGCTCTCTTTCTTTCTCCGT 8831
QY 1138 TTTTCTTTCTGCTCGGTCTCGATCTTTGCGCTTGTAGTTTGGGTGGGCGAGAGCGACT 1197
DB TTTTCTTTCTGCTCGGTCTCGATCTTTGCGCTTGTAGTTTGGGTGGGCGAGAGCGACT 8891
QY 1198 TCGTCCCGCAATGCGGTGCGCGGAGGCGGGAATCTCGCGCGTCTCCGGGGGCTG 1257
DB TCGTCCCGCAATGCGGTGCGCGGAGGCGGGAATCTCGCGCGTCTCCGGGGGCTG 8951
QY 1258 AGTCCGCGCGGATCTCGCGCGGGAATGGGCGTCTCGGATGTAGATCTCGCGCGCTT 1315
DB AGTCCGCGCGGATCTCGCGCGGGAATGGGCGTCTCGGATGTAGATCTCGCGCGCTT 9011
QY 1316 GTTGGGGGAGATGATGGGGCGTTTAAATTT-CGCCATGTCAACCAAGATCAGAGAGG 1374
DB GTTGGGGGAGATGATGGGGCGTTTAAATTTCCGCCATGTCAACCAAGATCAGAGAGG 9071
QY 1375 GGAAGAGGACATATGATATATTTATATATTTCTGCTGCGTCCGTCAGGCTTAGA 1434
DB GGAAGAGGACATATGATATATTTATATATTTCTGCTGCGTCCGTCAGGCTTAGA 9129
QY 1435 TGTGCTAGA--TCTTTCTTTCTTTTGTGGGTGAGAAATTTGAATCCCTCAGCATGT 1491
DB TGTGCTAGATCTTTCTTTCTTTCTTTTGTGGGTGAGAAATTTGAATCCCTCAGCATGT 9189

QY 1492 TCATCGGATGTTTCTTTTCATGATTTGACAAGATGACGCTCGGCGAGCTTTT 1551
DB TCATCGGATGTTTCTTTTCATGATTTGACAAGATGACGCTCGGCGAGCTTTT 9249
QY 1552 GTAGTAGACCATG 1565
DB GTAGTAGACCATG 9263
RESULT 5
AAT80053
ID AAT80053 standard; cDNA; 1392 BP.
XX
AC AAT80053;
XX
DT 25-MAR-2003 (revised)
DT 04-NOV-1997 (first entry)
XX
DE Rice actin 1 gene promoter fragment.
XX
KW Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;
KW cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.
XX
OS Oryza sativa.
XX
PN US5641876-A.
XX
PD 24-JUN-1997.
XX
PF 27-OCT-1993; 93US-00144602.
XX
PR 05-JAN-1990; 90US-00461490.
PR 18-SEP-1991; 91US-00762680.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Wu R, Mcelroy D;
XX
DR WPI; 1997-340996/31.
XX
PT Nucleic acid containing the promoter of the rice actin-1 gene - used to
PT direct efficient expression of foreign genes in rice.
XX
PS Claim 4; Col 35-38; 29pp; English.
XX
CC This sequence represents a fragment from the promoter region of the rice
CC actin-1 (Rac1) gene. Cytoplasmic actin is a fundamental and essential
CC component of the eukaryotic cell and cytoskeleton. In higher plant cells,
CC a number of cellular processes, such as cytoplasmic streaming, extension
CC growth and cell division are thought to involve the cytoskeletal actin
CC protein. All of the studied plant actins consist of four exons of
CC conserved length, separated by 3 introns of variable length. In rice
CC there are at least 8 actin-like sequences per haploid genome. Rac1
CC encodes a transcript that is relatively abundant in all rice tissues.
CC This sequence is an example of a nucleic acid molecule of the invention.
CC The nucleic acid molecules of the invention contain the Rac1 gene (or
CC fragments) with promoter activity in monocotyledonous plants. The
CC promoter is used to direct expression of foreign genes in transgenic rice
CC and other plants. The actin promoter is more efficient in rice
CC transformation than previously proposed promoters (e.g. 5 times more
CC active than the maize Adh1 promoter) and has constitutive activity in
CC space and time. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 1392 BP; 376 A; 343 C; 309 G; 364 T; 0 U; 0 Other;
Query Match 27.4%; Score 428.8; DB 2; Length 1392;
Best Local Similarity 84.9%; Pred. No. 1.1e-91;
Matches 518; Conservative 0; Mismatches 82; Indels 10; Gaps 3;
QY 958 CATGCATCACTGCGCAATCCCGCAAGAAATCAACACCTCCGATTCACGCTGCACCA 1017
DB CAAAGAAACGCCCGCCATCCGCACTATATACATACCCCGCTCTCCATCCCGCCA 894

```
QY 1018 ACTCGCCGCTCTCCGCGCCAGCACCAGAAAGATTGCGCGCCACCGCGGAGCTCTCC 1077
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 835 ACCCTACACACACACACACACACACACCTCCCTCCCTCGCTGCGGACACAGAGCTCTC 894
QY 1078 CCCCCCTCCCTCCGCGCGCGCGCGGTAACCAACCCCGC--CCCTCTCTCTTTCTTTCTCC 1135
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 895 CCCCCCTCCCTCCGCGCGCGCGGTAACCAACCCCGGCTCTCTCTCTTTCTTTCTCC 954
QY 1136 GTTTTCTTTTTCGCTCGCTCGCTGATCTTTGGCTTGTATGTTGGGTGGCGAAGCGG 1195
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 955 GTTTTCTTTTTCGCTCGCTCGCTGATCTTTGGCTTGTATGTTGGGTGGCGAAGAG--GCGG 1013
QY 1196 CTTCGTGCGCCAGATCGATCGCGGAGGCGGAGATCTCGCGGCTGCGCTCCGAGCG 1255
DB 1014 CTTCGTGCGCCAGATCGATCGCGGAGGCGGAGATCTCGCGGCTGCG-----GTCTC 1066
QY 1256 TGAGTCGCGCCGAGATCTCGCGGAGAAATGGGAGCTTCGATGTGATCTTGATCCGCGTT 1315
DB 1067 GCGGTGCGCGCGGATCTCGCGGAGAAATGGGAGCTTCGATGTGATCTTGATCCGCGTT 1126
QY 1316 GTTGGGGGAGATGATGAGGCGGTTTAAATTCGCCATGCTAAACAAGATCAGGAAGAGG 1375
DB 1127 GTTGGGGGAGATGATGAGGCGGTTTAAATTCGCCATGCTAAACAAGATCAGGAAGAGG 1186
QY 1376 GAAAAGGACATATGTTTATATTTTATATTTCTGCTGCTGCTGCTGAGGCTTAGAT 1435
DB 1187 GAAAAGGACATATGTTTATATTTTATATTTCTGCTGCTGCTGCTGAGGCTTAGAT 1246
QY 1436 GTGCTAGATCTTTCTTTCTTTCTTTTGTGGTAAATTTGAATCCCTCAGCATTTGTCAT 1495
DB 1247 GTGCTAGATCTTTCTTTCTTTCTTTTGTGGTAAATTTGAATCCCTCAGCATTTGTCAT 1306
QY 1496 CGGTAGTCTTTCTTTCTTTCTTTCTTTGTGACAAATGACAGCTCGGCGAGCTTTTGTAG 1555
DB 1307 CGGTAGTCTTTCTTTCTTTCTTTCTTTGTGACAAATGACAGCTCGGCGAGCTTTTGTAG 1366
QY 1556 GTAGACCATG 1565
DB 1367 GTAGGAAGATG 1376

RESULT 6
AAT80052
ID AAT80052 standard; cDNA; 2199 BP.
XX
AC AAT80052;
XX
DT 25-MAR-2003 (revised)
DT 04-NOV-1997 (first entry)
XX
DE Rice actin 1 gene promoter region.
XX
KW Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;
KW cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.
XX
OS Oryza sativa.
XX
PN US641876-A.
XX
PD 24-JUN-1997.
XX
PF 27-OCT-1993; 93US-00144602.
XX
PR 05-JAN-1990; 90US-00461490.
PR 18-SEP-1991; 91US-00762680.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Wu R, Mcelroy D;
XX
DR WPI; 1997-340996/31.
XX
PT Nucleic acid containing the promoter of the rice actin-1 gene - used to
```

```
PT direct efficient expression of foreign genes in rice.
XX
PS Claim 3; Col 33-36; 29pp; English.
XX
CC This sequence represents the promoter region from the rice actin-1 (Rac1)
CC gene. Cytoplasmic actin is a fundamental and essential component of the
CC eukaryotic cell and cytoskeleton. In higher plant cells, a number of
CC cellular processes, such as cytoplasmic streaming, extension growth and
CC cell division are thought to involve the cytoskeletal actin protein. All
CC of the studied plant actins consist of four exons of conserved length,
CC separated by 3 introns of variable length. In rice there are at least 8
CC actin-like sequences per haploid genome. Rac1 encodes a transcript that
CC is relatively abundant in all rice tissues. This sequence is an example
CC of a nucleic acid molecule of the invention. The nucleic acid molecules
CC of the invention contain the Rac1 gene (or fragments) with promoter
CC activity in monocotyledonous plants. The promoter is used to direct
CC expression of foreign genes in transgenic rice and other plants. The
CC actin promoter is more efficient in rice transformation than previously
CC proposed promoters (e.g. 5 times more active than the maize Adh1
CC promoter) and has constitutive activity in space and time. (Updated on 25
CC -MAR-2003 to correct PF field.)
XX
SQ Sequence 2199 BP; 603 A; 515 C; 446 G; 635 T; 0 U; 0 Other;
XX
Query Match 27.4%; Score 428.8; DB 2; Length 2199;
Best Local Similarity 84.9%; Pred. No. 1.3e-91;
Matches 518; Conservative 0; Mismatches 82; Indels 10; Gaps 3;
QY 958 CATTCGATCATCTGCCAATCCCCAGAAAATCAACACTCCCAATTCACGCTGCCACCA 1017
DB 1582 CAAAGAAAGCCCCCAGCCATGACATATACATACCCCCCTCTCTCCATCCCCCA 1641
QY 1018 ACTCCCGCTCTCCGCGCCACACCAAGAAATGGCGCGACCGCGGTGAGCTCTCC 1077
DB 1642 ACCCTACACACACACACACACACACTCTCTCCCTCGCTGCGGACACAGCTCTCTC 1701
QY 1078 CCCCCCTCCCTCCGCGCGCGCGGTAACCAACCCCGC--CCCTCTCTCTTTCTTTCTCC 1135
DB 1702 CCCCCCTCCCTCCGCGCGCGCGCGGTAACCAACCCCGCTCTCTCTTTCTTTCTCC 1761
QY 1136 GTTTTCTTTTTCGCTCGCTCGATCTTTGGCTTGTGATTTGGGTGGCGAAGCGG 1195
DB 1762 GTTTTCTTTTTCGCTCGCTCGATCTTTGGCTTGTGATTTGGGTGGCGAAG--GCGG 1820
QY 1196 CTTCGTGCGCCAGATCGATCGCGGAGGCGGAGATCTCGCGGCTCGCGGCG 1255
DB 1821 CTTCGTGCGCCAGATCGATCGCGGAGGCGGAGATCTCGCGGCTCGCGGCGG 1873
QY 1256 TGAGTCGCGCCGAGATCTCGCGGAGAAATGGGAGCTCTCGAGTGTATCTGATCCGCGTT 1315
DB 1874 GCGGTGCGCGCGGATCTCGCGGAGAAATGGGAGCTCTCGAGTGTATCTGATCCGCGTT 1933
QY 1316 GTTGGGGGAGATGATGAGGCGGTTTAAATTTGCCATGCTAAACAAGATCAGGAAGAGG 1375
DB 1934 GTTGGGGGAGATGATGAGGCGGTTTAAATTTGCCATGCTAAACAAGATCAGGAAGAGG 1993
QY 1376 GAAAAGGACATATGTTTATATTTTATATTTCTGCTGCTGCTCGCAGGCTTAGAT 1435
DB 1994 GAAAAGGACATATGTTTATATTTTATATTTCTGCTGCTGCTCGCAGGCTTAGAT 2053
QY 1436 GTGCTAGATCTTTCTTTCTTTTGTGGTATGTAATCCCTCAGCATTTGTCAT 1495
DB 2054 GTGCTAGATCTTTCTTTCTTTTGTGGTATGTAATCCCTCAGCATTTGTCAT 2113
QY 1496 CGGTAGTCTTTCTTTCTTTCTTTGTGACAAATGACAGCTCGTGGAGACTTTTGTAG 1555
DB 2114 CGGTAGTCTTTCTTTCTTTCTTTGTGACAAATGACAGCTCGTGGAGACTTTTGTAG 2173
QY 1556 GTAGACCATG 1565
DB 2174 GTAGGAAGATG 2183
```



```

RESULT 7
AA80055
ID   AAT80055 standard; cDNA; 5643 BP.
XX
AC   AAT80055;
XX
DT   25-MAR-2003 (revised)
DT   04-NOV-1997 (first entry)
XX
DE   Rice actin 1 gene.
XX
KM   Promoter: rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;
KM   cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.
XX
OS   Oryza sativa.
XX
PN   US5641876-A.
XX
PD   24-JUN-1997.
XX
PF   27-OCT-1993; 93US-00144602.
XX
PR   05-JAN-1990; 90US-00461490.
PR   18-SEP-1991; 91US-00762680.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Wu R, McElroy D;
XX
DR   WPI; 1997-340996/31.
XX
PT   Nucleic acid containing the promoter of the rice actin-1 gene - used to
PS   direct efficient expression of foreign genes in rice.
XX
XX   Example 1; Col 3-7; 29pp; English.
XX
CC   This sequence represents a the rice actin-1 (Rac1) gene amplified using
CC   AAT80054. Cytoplasmic actin is a fundamental and essential component of
CC   the eukaryotic cell and cytoskeleton. In higher plant cells, a number of
CC   cellular processes, such as cytoplasmic streaming, extension growth and
CC   cell division are thought to involve the cytoskeletal actin protein. All
CC   of the studied plant actins consist of four exons of conserved length,
CC   separated by 3 introns of variable length. In rice there are at least 8
CC   actin-like sequences per haploid genome. Rac1 encodes a transcript that
CC   is relatively abundant in all rice tissues. This sequence is an example
CC   of a nucleic acid molecule of the invention. The nucleic acid molecules
CC   of the invention contain the Rac1 gene, or fragments with promoter
CC   activity (see AAT80052 and AAT80053) in monocotyledonous plants. The
CC   promoter is used to direct expression of foreign genes in transgenic rice
CC   and other plants. The actin promoter is more efficient in rice
CC   transformation than previously proposed promoters (e.g. 5 times more
CC   active than the maize Adh1 promoter) and has constitutive activity in
CC   space and time. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 5643 BP; 1500 A; 1283 C; 1200 G; 1660 T; 0 U; 0 Other;
Query Match      27.4%; Score 428.8; DB 2; Length 5643;
Best Local Similarity 84.9%; Pred. No. 1.9e-91;
Matches 518; Conservative 0; Mismatches 82; Indels 10; Gaps 3;
QY   958 CATGCACTCACTGCGCAATGCCCAAAATCAACACCTCCCAATTCCACGCTGCCACCA 1017
DB   1585 CAAAGAAACGCCCCCAATCCCACTATATACATACCCCTCTCTCCATCCGCCCA 1644
QY   1018 ACTGCGCGCTCTCGCGGCAAGCAAGAAATGCGCGGCAACCGCGGAGAGCTCTC 1077
DB   1645 ACCCTACCAACACACCAACACCACTCTCTCTCGCTGCGGAGAGAGAGCTCTC 1704
QY   1078 CCCCCTCCCTCCGCGCGCGCGGTAACACACCCGCG--CCCTCTCTCTCTCTCTCTCC 1135
DB   1705 CCCCCTCCCTCCGCGCGCGCGGTAACACACCCGCGGCTCTCTCTCTCTCTCTCC 1764
QY   1136 GTTTTCTTTTCTGCTCGTCTGATCTTTGGCTTGAGTTGGTGGGCGAGAGCGG 1195

```

```

DB   1765 GTTTTCTTTTCCGCTCTGATCTTGAGCTTGATAGTTGGGGCGAGAG--GCGG 1823
QY   1196 CTTCGTGCGCCAGATCGGTGCGGAGGAGGAGATCTTCGCGGCTGCGCGGCG 1255
DB   1824 CTTCGTGCGCCAGATCGGTGCGGAGGAGGAGATCTTCGCGGCTGCG-----GTCYC 1876
QY   1256 TGAATCGCGCCGAGATCTCTCGCGGGAATGGGGCTCTCGGATGATATGATCCGCCGT 1315
DB   1877 GCGGTGCGCGCGGATCTCGCGGGAATGGGGCTCTCGGATGATATGATCCGCCGT 1936
QY   1316 GTTGGGGGAGATGATGAGGCGTTAAATTTTCGCATGCTAAACAAGATCAGAGAGG 1375
DB   1937 GTTGGGGGAGATGATGAGGCGTTAAATTTTCGCATGCTAAACAAGATCAGAGAGG 1996
QY   1376 GAAAGGGCACTATGTTTATATATTTTATATATTTTCTGCTGCTGCTCAGGCTTAGAT 1435
DB   1997 GAAAGGGCACTATGTTTATATATTTTATATATTTTCTGCTGCTGCTCAGGCTTAGAT 2056
QY   1436 GTGCTAGATCTTTCTTTCTTTTGTGGGTAAGAAATTTGAATCCTCAGCATTTTCAT 1495
DB   2057 GTGCTAGATCTTTCTTTCTTTTGTGGGTAAGAAATTTGAATCCTCAGCATTTTCAT 2116
QY   1496 CGGTAGTTTTTTCTTTTCATGATTTTGACAATGACGCTCGGCGGAGCTTTTGTAG 1555
DB   2117 CGGTAGTTTTTTCTTTTCATGATTTTGACAATGACGCTCGGCGGAGCTTTTGTAG 2176
QY   1556 GTAGACCATG 1565
DB   2177 GTAGAGATG 2186

RESULT 8
AAZ47117
ID   AAZ47117 standard; DNA; 623 BP.
XX
AC   AAZ47117;
XX
DT   15-MAR-2000 (first entry)
XX
DE   Rice Act1-GUS fusion gene 5' transcribed region.
XX
KM   Transformation; transgenic plant; pineapple; tociopotent body; resistance;
KM   pest; disease; maize; sucrose phosphate synthase; enzyme; sweetness;
KM   thauanatin; antisense; inhibition; gene expression; ACC synthase; actin;
KM   fruit ripening; polyphenol oxidase; browning reaction; chilling injury;
KM   rice; beta-glucuronidase; ss.
XX
OS   Synthetic.
XX
FH   Key Location/Qualifiers
FT   TATA_signal 3..8
FT   exon 42..120
FT   exon 42..120
FT   exon 42..120
FT   misc_RNA 42
FT   intron 121..568
FT   intron 121..568
FT   exon 569..623
FT   CDS 576..623
FT   /*tag= f
FT   /product= "N-terminal 16 amino acids of GUS protein"
XX
XX   WO958644-A1.
XX
PD   18-NOV-1999.
XX
PF   13-MAY-1999; 99MO-US010576.

```

XX 14-MAY-1998; 98US-00078862.
PR (UTMA-) UNIV HAWAII.
XX Nan G, Nagai C;
XX WPI; 2000-062292/05.
DR P-PSDB; AAY56018.
XX
XX Stably transformed transgenic pineapple-like totipotent body and plants,
PT methods of transformation and culture.
XX
XX Example 2; Fig 3; 87pp; English.
XX
XX The invention relates to the generation of a stably transformed
CC transgenic pineapple-like totipotent body. The methods are used for the
CC production of transgenic pineapple-like totipotent bodies, and in
CC particular, transgenic plants derived from them. The plants can be
CC engineered to exhibit resistance to pests and disease and to exhibit
CC improved qualities. The transgenic bodies can be transformed with
CC constructs containing genes of interest as the maize sucrose phosphate
CC synthase enzyme (Genbank accession m9750) or a sweetness protein (e.g.
CC chaumatin) to increase the sweetness of the fruit. Alternatively,
CC constructs can include antisense sequences to inhibit gene expression,
CC e.g. an antisense construct to ACC synthase, which would delay fruit
CC ripening or to polyphenol oxidase (Genbank accession s40548) which would
CC prevent the browning reaction occurs during chilling injury. The
CC expression construct comprises promoter which drives the expression of
CC the gene of interest. This sequence represents an example of a construct
CC and comprises the 5' transcribed region of the rice actin-1 gene linked
CC to the beta-glucuronidase enzyme coding sequence
XX
SQ Sequence 623 BP; 98 A; 184 C; 164 G; 177 T; 0 U; 0 Other;

Query Match 27.2%; Score 426.2; DB 3; Length 623;
Best Local Similarity 87.3%; Pred. No. 3.4e-91;
Matches 504; Conservative 0; Mismatches 63; Indels 10; Gaps 3;
QY 991 ACACCTCCCAATTCACGCTGCGACCAACGCGCTCTCCGCGCAAGCAACCAAGGAA 1050
DB 10 ACCCCCCCTCTCTCCATCCCCCAACCTACCAACACACACACACCTCTCTCC 69
QY 1051 TTGGCCGCCACCGCGGAGAGCTCTCCCTCCCTCCGCGCGCGCGCGGTAAACACC 1110
DB 70 CCTCTGCTGCGGACGACGAGCTCTCTCCCTCTCCCTCTCCGCGCGCGCGGTAAACACC 129
QY 1111 CCGC--CCCT 1168
DB 130 CCGCGTCCCT 189
QY 1169 CTGTGTAGTTGGGTGGGCGAGAGCGGCTTCTGTCGCCAGATCGTGGCGGAGGCGG 1228
DB 190 CTGTGTAGTTGGGCGGAGAG--GCGGCTTCTGTCGCCAGATCGTGGCGGAGGCGG 248
QY 1229 GGAATCGGCGGCTGGGGTCTCCGGGGGTGAGTGGCGCGGATCCTCGCGGGGAAATGGGCG 1288
DB 249 GGAATCGGCGGCTGGG-----GTCTCGGCGTGGCGGCGGATCTCGCGGGAATGGGCG 301
QY 1289 TCTCGGATGTAGATCTGATCCGCGTGTGTGGGCGAGATGATGATGATTAATTTTCG 1348
DB 302 TCTCGGATGTAGATCTGATCCGCGTGTGTGGGCGAGATGATGATGATTAATTTTCG 361
QY 1349 CCATGTAAACAAGATCAGGAAGGAGGAAAAGGCGCTATGTGTTATATTTTATATAT 1408
DB 362 CCATGTAAACAAGATCAGGAAGGAGGAAAAGGCGCTATGTGTTATATTTTATATAT 421
QY 1409 TTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1468
DB 422 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
QY 1469 GAATTTGAATCCTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTTGACAAAT 1528

DB 482 GAATTTGAATCCTCAGCATTTGTCATCGGTAGTTTCTTTTCATGATTTTGACAAAT 541
QY 1529 GCAGCTGTGCGGAGCTTTTGTAGGTAGCAATG 1565
DB 542 GCAGCTGTGCGGAGCTTTTGTAGGTAGCAATG 578

RESULT 9
ABK86738
ID ABK86738 standard; DNA; 623 BP.
XX
XX ABK86738;
XX
XX 24-SEP-2002 (first entry)
XX
XX

DE Rice Act1 gene.

KW Rice; gene; db; transgenic; plant; lignocellulose; cellulase; ligninase;
KW fermentable sugar; ethanol; fermentation; silage; feed; fuel;
KW industrial chemical; biodegradation; chloroaromatic;
KW environmental pollutant; Act1.

OS Oryza sativa.

PN WO200234926-A2.

PD 02-MAY-2002.

PF 18-OCT-2001; 2001WO-US032538.

PR 20-OCT-2000; 2000US-0242408P.

XX (UNMS) UNIV MICHIGAN STATE.

PI Sticklen MB, Dale BE, Magpool S;

DR WPI; 2002-489947/52.

PT Producing transgenic plants which after harvest degrade lignin and
PT cellulose to fermentable sugars, by mating transgenic plant comprising
PT DNA encoding cellulase with transgenic plant comprising DNA encoding
PT ligninase.
XX
XX

PS Example 1; Page 124; 126pp; English.

CC The invention discloses the production of a transgenic plant which
CC degrades lignocellulose when the plant is ground. It comprises the
CC production of the transgenic plant including cellulase and ligninase by
CC mating a transgenic plant, containing a DNA encoding a cellulase, and a
CC transgenic plant, containing a DNA encoding a ligninase, where both genes
CC are operably linked to a nucleotide sequence encoding a signal peptide
CC which targets the fusion protein to an organelle of the plant,
CC particularly chloroplasts. The method is useful for producing a
CC transgenic plant (e.g. maize) which degrades lignocellulose when the
CC plant is ground to produce a plant material. This material is useful for
CC converting lignocellulose, in a plant material, to fermentable sugars
CC which are then fermented to ethanol. The transgenic plants also provide a
CC plentiful and inexpensive source of fungal or bacterial cellulases and
CC ligninases which can be used in the production of ethanol. They can also
CC be used for pre-treating silage to increase the energy value of
CC lignocellulosic feeds for cows and other ruminant animals, pre-treating
CC lignocellulosic biomass for fermentative conversion to fuels and
CC industrial chemicals, and biodegradation of chloroaromatic environmental
CC pollutants. The sequence presented is the rice Act1 gene and promoter
XX
SQ Sequence 623 BP; 98 A; 184 C; 164 G; 177 T; 0 U; 0 Other;

Query Match 27.2%; Score 426.2; DB 6; Length 623;
Best Local Similarity 87.3%; Pred. No. 3.4e-91;
Matches 504; Conservative 0; Mismatches 63; Indels 10; Gaps 3;
QY 991 ACACCTCCCAATTCACGCTGCGACCAACGCGCTCTCCGCGCAAGCAACCAAGGAA 1050

```
Db 10 ACCCCCCCTCTCTCCATCCCCCAACCTACACACACACACACACTCTCTCCC 69
Qy 1051 TTGGCCGCGACCGGGGTGAGCTCTCTCCCTCCCTCCGCGCGGGTAACACC 1110
Db 70 CCCTGCGTCCGCGAGCAGACGACTCTCTCCCTCCCTCCGCGCGGGTAACACC 129
Qy 1111 CCGC--CCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1168
Db 130 CCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 189
Qy 1169 CTTGTGATTTGGGTGGGCGAGACGCGCTTCTGTCGCCAGATCGGCGGAGGGCG 1228
Db 190 CTTGTGATTTGGGCGGCGAGG--GCGGCTTCTGTCGCCAGATCGGCGGAGGGCG 248
Qy 1229 GGAATCTCGCGGCTGCGCTCTCTCGGCGCTGAGTCTGCGCGGAAATGCGGC 1288
Db 249 GGAATCTCGCGGCTGCG-----GTCTCGGCGTGGCGCGGATCTCTCGCGGGAATGCGGC 301
Qy 1289 TCTGCGATGATGATCTGATCCGCGCTTGTGGGGAGATGATGGGGGCTTAAATTCG 1348
Db 302 TCTGCGATGATGATCTGATCCGCGCTTGTGGGGAGATGATGGGGGCTTAAATTCG 361
Qy 1349 CCATGCTAAACAAGATCAGAAAGAGGGAAGGCACTATGTTATTTATTTATTTAT 1408
Db 362 CCATGCTAAACAAGATCAGAAAGAGGGAAGGCACTATGTTATTTATTTATTTAT 421
Qy 1409 TTTGCTGCTGCTGCTGCTGAGGCTTATGATGCTTCTCTCTCTCTCTCTCT 1468
Db 422 TTTGCTGCTGCTGCTGCTGAGGCTTATGATGCTTCTCTCTCTCTCTCTCTCT 481
Qy 1469 GAATTTGAATCCCTCAGATCTTATCATCGATGTTTCTTTTCTTATGATTTGACAAT 1528
Db 482 GAATTTGAATCCCTCAGATCTTATCATCGATGTTTCTTTTCTTATGATTTGACAAT 541
Qy 1529 GCAGCTCTGTCGAGGCTTTTGTAGGTAGACCATG 1565
Db 542 GCAGCTCTGTCGAGGCTTTTGTAGGTAGACCATG 578

RESULT 10
AAF80289 ID AAF80289 standard; DNA; 7943 BP.
XX AAF80289;
AC AAF80289;
XX
DT 29-JUN-2001 (first entry)
XX
DE Nucleotide sequence of plasmid pMR1201.
XX
KM Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KM P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT rep_origin 1..654
FT /tag= a
FT /note= "ori RK2"
FT 655..1263
FT /tag= b
FT /note= "ori ColEI"
FT 1264..2603
FT /tag= c
FT /note= "NPT III gene coding for neomycin
FT phosphotransferase and kanamycin resistance"
FT 2604..4098
FT CDS
FT /tag= d
FT /note= "trfA locus from RK2 coding for two proteins P285
FT and P382 enabling an increase in the replication rate"
FT 4106..4271
FT /tag= e
FT /note= "T-DNA left border"
FT 4272..4559
FT terminator
```

```
FT FT /*tag= f
FT FT /note= "nopaline synthetase terminator"
FT FT 4612..5047
FT FT /tag= g
FT FT /note= "Wheat high molecular weight glutenin promoter"
FT FT 5096..5627
FT FT /tag= h
FT FT /note= "rice actin intron"
FT FT 5628..7436
FT FT /tag= i
FT FT /note= "GUS gene coding for beta glucuronidase"
FT FT 7437..7763
FT FT /tag= j
FT FT /note= "nopaline synthetase terminator"
FT FT 7763..7936
FT FT /tag= k
FT FT /note= "T-DNA right border"
XX
PN FR2798139-A1.
XX
XX 09-MAR-2001.
XX
XX 03-SEP-1999; 99FR-00011112.
XX
XX 03-SEP-1999; 99FR-00011112.
XX
XX (MERI-) MERISTEM THERAPEUTICS SA.
XX
XX PI Gruber V, Comeau D;
XX
XX WPI; 2001-259847/27.
XX
XX New vector free from non-essential elements, useful for transforming
XX cells for protein production and for preparing transgenic plants.
XX
XX Claim 20; Page 137-140; 180pp; French.
XX
XX The specification describes a synthetic vector containing only those
XX elements essential for its functionality and transgenesis of a cell
XX (especially a plant cell). The vector consists of at most one origin of
XX replication (ori), at most one sequence encoding a selection agent and a
XX trfA locus encoding a protein that increases the level of plasmid
XX replication. The vector particularly contains an RK2 ori, especially oriV
XX from pRK2 of Escherichia coli with a broad host range, an antibiotic
XX resistance gene (especially nptIII conferring resistance to kanamycin in
XX bacteria) and a trfA locus from pRK2 encoding the proteins P285 and P382.
XX The vectors are used to prepare transgenic plants and transformed host
XX cells for production of a heterologous proteins, e.g. insulin.
XX interferon, lipase, blood proteins and anti-inflammatory agents. The
XX present sequence represents a plasmid of the invention
XX
SQ Sequence 7943 BP; 2006 A; 1955 C; 2139 G; 1843 T; 0 U; 0 Other;

Query Match 25.0%; Score 392; DB 4; Length 7943;
Best Local Similarity 93.0%; Pred. No. 1,2e-82;
Matches 491; Conservative 0; Mismatches 20; Indels 17; Gaps 7;

Qy 1053 GGGCGGACCGGCGTGAAGCTCTCCCTCCCTCCGCGCGC-----CGCGGTAAAC 1107
Db 5071 GGGCGGACCGGCGTGAAGCTCTCCCTCCCTCCGCGCGCGCGGTAAAC 5130
Qy 1108 ACCCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1166
Db 5131 ACCCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5190
Qy 1167 GCCTGTGATTTGGGTGGGCGGCGAGA-----GCGGCTCTGTCGCCAGATGGGCGGA 1222
Db 5191 GCCTGTGATTTGGGTGGGCGGCGAGCGGCTTCTGTCGCCAGATGCTGCGGGA 5250
Qy 1223 GGGCGGAGATCTGCGGCTTCTCTCG--GGCGTGAATCGGCGCGGATCTCGCGGG 1280
Db 5251 GGGCGGAGATCTGCGGCTTCTCTCGCGCGCGGTGAATCGGCGCGGATCTCGCGGG 5310
```

```

QY 1281 AATGGGCTCTCGGATGATGCT--GATCCGCGTGTGTGGGGAGATGATGGGGGTT 1338
    |||||
DB 5311 AATGGGCTCTCGGATGATGCTGCGATCCGCCGTTGTGGGGAGATATGGGGGTT 5370
    |||||
QY 1339 TAAATTTT--CGCATGCTTAAACAAGATCAGAGAGAGGAGAAAGGCACTATGCTTTATA 1397
    |||||
DB 5371 TAAATTTTCCGATGCTTAAACAAGATCAGAGAGAGGAGAAAGGCACTATGCTTTATA 5430
    |||||
QY 1398 TTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457
    |||||
DB 5431 TTTTATATATTTCTGCTGCT--TCGTCAGGCTTAGATGCTAGATCTTTCTTCTCT 5488
    |||||
QY 1458 TTTTGGGAGTAGAATTGATCCCTCAGATTGCTATCGGTAGTTTCTTTTCATGAT 1517
    |||||
DB 5489 TTTTGGGAGTAGAATTGATCCCTCAGATTGCTATCGGTAGTTTCTTTTCATGAT 5548
    |||||
QY 1518 TTGTGACAAATGACAGCTCGTGGAGCTTTTGTAGTAGACCATG 1565
    |||||
DB 5549 TTGTGACAAATGACAGCTCGTGGAGCTTTTGTAGTAGACCATG 5596
    |||||

RESULT 11
AAFB0286
ID AAFB0286 standard; DNA; 9143 BP.
XX
XX AAFB0286;
AC
XX
XX 29-JUN-2001 (first entry)
XX
XX Nucleotide sequence of plasmid pMR1193.
XX
XX Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KM P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
XX
XX Synthetic.
XX
XX Key rep_origin
FH Location/Qualifiers
FT 1..654
FT /*tag= a
FT /note= "ori RK2"
FT 655..1263
FT /*tag= b
FT /note= "ori COLE1"
FT 1264..2603
FT /*tag= c
FT /note= "NPT III gene coding for neomycin
FT phosphotransferase and kanamycin resistance"
FT 2604..4098
FT /*tag= d
FT /note= "TrfA locus from RK2 coding for two proteins P285
FT and P382 enabling an increase in the replication rate"
FT 4106..4271
FT /*tag= e
FT /note= "T-DNA left border"
FT 4272..4559
FT /*tag= f
FT /note= "NPT III gene coding for neomycin
FT phosphotransferase and kanamycin resistance"
FT 4560..5557
FT /*tag= g
FT /note= "NPT III gene coding for neomycin
FT phosphotransferase and kanamycin resistance"
FT 5557..5770
FT /*tag= h
FT /note= "nopaline synthetase promoter"
FT 5829..6254
FT /*tag= i
FT /note= "high molecular weight glutenin promoter from
FT wheat"
FT 6301..6833
FT /*tag= j
FT /note= "rice actin intron"
FT 6834..8643
FT /*tag= k

```

```

FT /*note= "GUS gene coding for beta glucuronidase"
FT 8644..8959
FT /*tag= l
FT /note= "nopaline synthetase terminator"
FT 8959..9136
FT /*tag= m
FT /note= "T-DNA right border"
PN FR2798139-A1.
XX
XX 09-MAR-2001.
PD
XX
XX 03-SEP-1999; 99FR-00011112.
XX
XX 03-SEP-1999; 99FR-00011112.
PR
XX (MER1-) MERISTEM THERAPEUTICS SA.
XX
XX Gruber V, Comeau D;
XX
XX MPI; 2001-259847/27.
DR
XX
XX New vector free from non-essential elements, useful for transforming
XX cells for protein production and for preparing transgenic plants.
XX
XX Claim 20; Page 124-127; 180pp; French.
XX
XX The specification describes a synthetic vector containing only those
XX elements essential for its functionality and transgenesis of a cell
XX (especially a plant cell). The vector consists of at most one origin of
XX replication (ori), at most one sequence encoding a selection agent and a
XX trfA locus encoding a protein that increases the level of plasmid
XX replication. The vector particularly contains an RK2 ori, especially oriV
XX from pRK2 of Escherichia coli with a broad host range, an antibiotic
XX resistance gene (especially nptIII conferring resistance to kanamycin in
XX bacteria) and a trfA locus from pRK2 encoding the proteins P285 and P382.
XX The vectors are used to prepare transgenic plants and transformed host
XX cells for production of a heterologous proteins, e.g. insulin,
XX interferon, lipase, blood proteins and anti-inflammatory agents. The
XX present sequence represents a plasmid of the invention
XX
XX Sequence 9143 BP; 2284 A; 2299 C; 2479 G; 2081 T; 0 U; 0 Other;
SQ
Query Match 25.0%; Score 392; DB 4; Length 9143;
Best Local Similarity 93.0%; Pred No. 1.3e-82;
Matches 491; Conservative 0; Mismatches 20; Indels 17; Gaps 7;
QY 1053 GGGCGGACCGCGGTGAGCTCTCCCTCCCTCCCTCCGCGC-----CGCCGTAACC 1107
    |||||
DB 6278 GGGCGGACCGCGGTGAGCTCTCCCTCCCTCCCTCCGCGCGCGCGCGGTAACC 6337
    |||||
QY 1108 ACCCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1166
    |||||
DB 6338 ACCCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6397
    |||||
QY 1167 GCCTGTGATTTGGGTGGGCGAGA---GCGGCTTCGTCGCGCAATCGTGCGCGGA 1222
    |||||
DB 6398 GCCTGTGATTTGGGTGGGCGAGA---GCGGCTTCGTCGCGCGCAATCGTGCGCGGA 6457
    |||||
QY 1223 GGGCGGAGTCTCGCGCTGCGCTCGC--GCGTGAATCGGCCCGATCTCGCGGG 1280
    |||||
DB 6458 GGGCGGAGTCTCGCGCTGCGCGCTCGC--GCGTGAATCGGCCCGATCTCGCGGG 6517
    |||||
QY 1281 AATGGGCTCTCGGATGATGCT--GATCCGCGTGTGTGGGGAGATGATGGGGGTT 1338
    |||||
DB 6518 AATGGGCTCTCGGATGATGCT--GATCCGCGTGTGTGGGGAGATGATGGGGGTT 6577
    |||||
QY 1339 TAAATTTT--CGCATGCTTAAACAAGATCAGAGAGAGGAGAAAGGCACTATGCTTTATA 1397
    |||||
DB 6578 TAAATTTTCCGATGCTTAAACAAGATCAGAGAGAGGAGAAAGGCACTATGCTTTATA 6637
    |||||
QY 1398 TTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457
    |||||

```

Db 6638 TTTTATATATTTCTGTCGT--TCGTCAGGCTTAGATGAGCTAGATCTTTCTTCTCT 6695
QY 1458 TTTTGGGGTGAATTGAAATCCCTCAGCATGTTCAATCGGTAGTTTCTTTTCATGAT 1517
Db 6696 TTTTGGGTGAAGATTGAATCCCTCAGCATGTTCAATCGGTAGTTTCTTTTCATGAT 6755
QY 1518 TTGTGAACAATGACGCTCGTGGGAGCTTTTGTGTGGTAGACCATG 1565
Db 6756 TTGTGAACAATGACGCTCGTGGGAGCTTTTGTGTGGTAGACCATG 6803

RESULT 12
AAF80295
ID AAF80295 standard; DNA, 10003 BP.
AC AAF80295;
XX
XX 29-JUN-2001 (first entry)
XX
XX Nucleotide sequence of plasmid pMRT1210.
XX
XX Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KM P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
XX
XX Synthetic.
XX
XX Key
FH rep_origin
FT Location/Qualifiers
FT 1..654
FT /tag= a
FT /note= "ori RK2"
FT 655..1263
FT /tag= b
FT /note= "ori COLE1"
FT 1264..2603
FT /tag= c
FT /note= "NPT III gene coding for neomycin
phosphotransferase and kanamycin resistance"
FT 2604..4098
FT /tag= d
FT /note= "trfA locus from RK2 coding for two proteins P285
and P382 enabling an increase in the replication rate"
FT 4106..4271
FT /tag= e
FT /note= "T-DNA left border"
FT 4272..4559
FT /tag= f
FT /note= "nopaline synthetase terminator"
FT 4594..5169
FT /tag= g
FT /note= "Bar gene coding for phosphinotricin
acetyltransferase and glufosinate resistance"
FT 5170..5704
FT /tag= h
FT /note= "rice actin intron"
FT 5705..6638
FT /tag= i
FT /note= "rice actin promoter"
FT 6672..7107
FT /tag= j
FT /note= "wheat high molecular weight glutenin promoter"
FT 7169..7687
FT /tag= k
FT /note= "rice actin intron"
FT 7688..9496
FT /tag= l
FT /note= "GUS gene coding for beta glucuronidase"
FT 9497..9823
FT /tag= m
FT /note= "nopaline synthetase terminator"
FT 9823..9996
FT /tag= n
FT /note= "T-DNA right border"
XX

PN FR2798139-A1.
XX
XX PD 09-MAR-2001.
XX
XX PF 03-SEP-1999; 99FR-00011112.
XX
XX PR 03-SEP-1999; 99FR-00011112.
XX
XX (MER1-) MERISTEM THERAPEUTICS SA.
XX
XX Gruber V; Comeau D;
XX
XX WPI; 2001-259847/27.
XX
XX PT New vector free from non-essential elements, useful for transforming
XX cells for protein production and for preparing transgenic plants.
XX
XX PS Claim 20; Page 163-166; 180pp; French.
XX
XX The specification describes a synthetic vector containing only those
XX elements essential for its functionality and transgenesis of a cell
XX (especially a plant cell). The vector consists of at most one origin of
XX replication (ori), at most one sequence encoding a selection agent and a
XX trfA locus encoding a protein that increases the level of plasmid
XX replication. The vector particularly contains an RK2 ori, especially oriV
XX from pRK2 of *Escherichia coli* with a broad host range, an antibiotic
XX resistance gene (especially nptIII conferring resistance to Kanamycin in
XX bacterial) and a trfA locus from pRK2 encoding the proteins P285 and P382.
XX The vectors are used to prepare transgenic plants and transformed host
XX cells for production of a heterologous proteins, e.g. insulin.
XX interferon, lipase, blood proteins and anti-inflammatory agents. The
XX present sequence represents a plasmid of the invention
XX

SQ Sequence 10003 BP; 2476 A; 2470 C; 2729 G; 2328 T; 0 U; 0 Other;
Query Match 25.0%; Score 392; DB 4; Length 10003;
Best Local Similarity 93.0%; Pred. NO. 1.4e-82;
Matches 491; Conservative 0; Mismatches 20; Indels 17; Gaps 7;
QY 1053 GGCGGACACGCGGAGAGCTCTCCCTCCCTCCGCGC-----CGCGGTAAAC 1107
Db 7131 GGCGGACACGCGGAGAGCTCTCCCTCCCTCCGCGCGCGCGCGGTAAAC 7190
QY 1108 ACCCGCCCT 1166
Db 7191 ACCCGCCCT 7250
QY 1167 GCCTTGATGTTGGGTGGGCGA----CGCGCTTCGTCCGCAATGCGGCGGGA 1222
Db 7251 GCCTTGATGTTGGGTGGGCGAAGAGCGGCTTCGTCCGCGCAATGCGGCGGGA 7310
QY 1223 GGGGCGGAGTCTCGCGGCTGCGCTCCG--GGCGTGAATCGGCGCGATCTCGCGGG 1280
Db 7311 GGGGCGGAGTCTCGCGGCTGCGGCTCTCGCGCGGTGAATCGGCGCGATCTCGCGGG 7370
QY 1281 AATGGGCTCTCGGATGATGATCT--GATCCGCGTGTGTGGGAGATGATGAGGCGGT 1338
Db 7371 AATGGGCTCTCGGATGATGATGATCGGCGCGCGTGTGTGGGAGATGATGAGGCGGT 7430
QY 1339 TAAATTTT--CGCATCTTAAACAAGATCAGAAAGAGGGAAGGACATATGTTTAT 1397
Db 7431 TAAATTTTCCGCATCTTAAACAAGATCAGAAAGAGGGAAGGACATATGTTTAT 7490
QY 1398 TTTTATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457
Db 7491 TTTTATATATTTCTGCTGCT--TCGTCAGGCTTATATGATGATCTTTCTTTCTTCT 7548
QY 1458 TTTTGGGTGAATTTGAATCCCTCAGCATGTTCAATCGGTAGTTTCTTTTCATGAT 1517
Db 7549 TTTTGGGTGAATTTGAATCCCTCAGCATGTTCAATCGGTAGTTTCTTTTCATGAT 7608
QY 1518 TTGTGAACAATGACGCTCGTGGGAGCTTTTGTGTGGTAGACCATG 1565

Dd		7699	TTGTGACAAATGCAGCCTTCGTGGCGAGCTTTTTTGTAGTAGACCATTG	7656
			RESULT_13	
			ID ABT07357 standard; DNA; 470 BP.	
XX	XX	ABT07357		
AC	XX	ABT07357;		
DT	XX	07-NOV-2002 (first entry)		
DE	XX	Reporter construct fragment rice actin intron SEQ ID NO: 109.		
XX	XX	Plant; gene expression control; insect; hormone receptor; fertility;		
KW	XX	ecdysone receptor; ds.		
OS	XX	Oryza sativa.		
FN	XX	WO200261102-A2.		
PD	XX	08-AUG-2002.		
PF	XX	24-OCT-2001; 2001WO-US051417.		
XX	XX	24-OCT-2000; 2000US-0242969P.		
PR	XX	(SYGN) SYNGENTA PARTICIPATIONS AG.		
PA	XX	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;		
PI	XX	WPI; 2002-619259/66.		
DR	XX	New receptor cassette encoding a chimeric receptor polypeptide, useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility.		
PT	XX	Example 10; Page 263; 319pp; English.		
PS	XX	The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecdysone receptor (ECR) of an insect, a ligand binding domain of an insect ECR, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The present sequence is a polynucleotide described in the exemplification of the invention		
CC	XX			
CC	XX			
SQ	XX	Sequence 470 BP; 75 A; 103 C; 141 G; 151 T; 0 U; 0 Other;		
		Query Match 24.9%; Score 390.4; DB 6; Length 470;		
		Best Local Similarity 93.9%; Pred. No. 1e-82;		
		Matches 443; Conservative 0; Mismatches 16; Indels 13; Gaps 3;		
QY		1099 CGGTAACACACCCGCCCTCTCCCTCTTCTTCTTGCGTTTTTTTTT-CGTCGGGCT	1157	
Dd		1 CGGTAAACACCCGCCCTCTCTCTTCTTCTTGCGTTTTTTTTTTCGCTCGGCT	60	
QY		1158 CGATCTTGGCCTTGGAATTGGGTGGGCGAGA---GCGGCTTCGTGCCCAAGATCG	1213	
Dd		61 CGATCTTGGCCTTGGAATTGGGTGGGCGAGA---GCGGCTTCGTGCCCAAGATCG	120	
QY		1214 TGCGGGGAGGGGCGGGAATCTGCGGGCTGGCGCTCTCGGGCGTGAAGTGGCCCCGGAATCT	1273	
Dd		121 TGCGGGGAGGGGCGGGAATCTGCGGGCTGGCGCTCTCGGGCGTGAAGTGGCCCCGGAATCT	172	
QY		1274 CGCGGGGAATGGGGGCTTCGGAATGTAATCGATCGCGGTGTTGGGGGAGATGATGGG	1333	
Dd		173 CGCGGGGAATGGGGGCTTCGGAATGTAATCGATCGCGGTGTTGGGGGAGATGATGGG	232	
QY		1334 GCCTTTAAATTCGCTCATGTCTAACAAGATCAGGAMAAGGGGAAACTATGTT	13933	

Db	233	GGCTTTAAATTTGGCATGCTAAACAAGATCAGGAAGAGGGGAAAAGGCCATATGGTT	292
Oy	1394	TAAATTTTAAATATATTTCTGCTGCTGCTCGTCAAGCTTAATGTGCTAAGATCTTTCTTTTC	1453
Db	293	TAAATTTTAAATATATTTCTGCTGCTGCTCGTCAAGGCTTAAGATGTGCTAAGATCTTTCTTTTC	352
Oy	1454	TTCTTTTGGGGAGAAATTTGGAATCCCTCAGCATTTTTCATCGATCGATGTTTCTTTTCA	1513
Db	353	TTCTTTTGGGGAGAAATTTGGAATCCCTCAGCATTTTTCATCGATGTTTCTTTTCTTTTCA	412
Oy	1514	TGAATTTGACAAATGACGCTCGTGGGAGACTTTTGTAGGTAGACCAATG	1565
Db	413	TGAATTTGACAAATGACGCTCGTGGGAGACTTTTGTAGGTAGAGAGCTG	464

XX	RESULT 14
XX	ID ADF49181
XX	ADFA9181 standard; DNA; 470 BP.
XX	AC
XX	ADFA9181;
XX	12-FEB-2004 (first entry)
XX	DE Rice actin intron.
XX	receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW	hinge domain; ecdysonic receptor; EcdR ligand binding domain;
KW	activation domain; transgenic seed; transgenic plant; plant line;
KW	herbicide; pesticide; rice; actin; intron; ds.
XX	
OS	Oryza sp.
XX	
PN	US2003154509-A1.
XX	
PD	14-AUG-2003.
XX	
PF	24-OCT-2001; 2001US-00087167.
XX	
PR	24-OCT-2001; 2001US-00087167.
XX	
PA	(PASC/) PASCAL E J.
PA	(VALE/) VALENTINE S A.
PA	(BROW/) BROWN J A.
PA	(COCK/) COCKRELL A S.
PA	(JOHN/) JOHNSON B D.
XX	
FI	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX	
DR	WPI; 2003-897756/82.
XX	
PT	New receptor cassette encoding a chimeric receptor polypeptide, useful
PT	for regulating the expression of target polypeptides in plants in the
PT	presence of appropriate chemical ligands.
XX	
XX	Example 10; SEQ ID NO 109; 186bp; English.
XX	
XX	The invention describes a receptor cassette encoding a chimeric receptor
CC	polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
CC	(D) domain of an ecdysonic receptor (EcdR) of an insect, a ligand binding
CC	(E) domain that is heterologous with respect to the D domain, and an
CC	activation domain. The receptor cassette and method are useful in
CC	regulating the expression of target polypeptides in plants in the
CC	presence of appropriate chemical ligands. The transgenic seeds and plants
CC	can be used for the breeding of improved plant lines that, for e.g.,
CC	increase the effectiveness of conventional methods such as herbicide or
CC	pesticide treatment. This sequence represents a rice actin intron used in
CC	the construction of a monocot-expressible target expression cassette
CC	comprising the firefly luciferase reporter gene and having response
CC	elements for the GAL4 DNA binding domain.
XX	
XX	Sequence 470 BP; 75 A; 103 C; 141 G; 151 T; 0 U; 0 Other;

Db 8064 TCGTCGCGAGCTTTTGTAGTAGACC 8091

Search completed: September 12, 2005, 00:41:11
Job time : 671.718 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 23:36:11 ; Search time 4105.12 Seconds
(without alignments)
14511.284 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565
Sequence: 1 GAATTCCTGAGGTGACGCG.....TTTTGTAGTAGACCAAG 1565

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	222	14.2	776	9	CG005206 ZUAE955TH
2	221.2	14.1	293	8	CC001894 PUBBC30TD
3	218.8	14.0	853	8	BZ791049 PUGD01TB
4	218.8	14.0	864	8	BZ808218 PUGC02TB
5	218.4	14.0	838	9	CG018790 ZUAE66TH
6	218	13.9	1008	9	CL998388 ZMABH001
7	217.2	13.9	1026	9	CL998109 ZMABH001
8	217.2	13.9	927	6	CD437903 EL01N0506
9	217.2	13.9	861	6	CD437683 EL01N0506
10	216.4	13.8	988	9	CL988337 ZMABH000
11	216.2	13.8	807	9	CG152598 PULH31TD
12	215.6	13.8	728	9	CM015128 ZMABH000
13	215.6	13.8	874	9	CG196646 PUDR84TB
14	214.4	13.7	646	9	CG082637 PULB06TD
15	214	13.7	890	8	BZ674680 PUBEO2TD
16	213.2	13.6	929	9	CG711569 OGLCB93TH
17	213.2	13.6	1025	9	CL998355 ZMABH001
18	213	13.6	782	9	CG347502 OGD719TV
19	213	13.6	927	9	CG172605 PUFJ32TB
20	212.2	13.6	786	8	BZ978385 PUGIX48TD
21	212.2	13.6	982	9	CG152241 PUGDM51TD
22	211.8	13.5	944	8	CG338516 OGBG42TV
23	211	13.5	668	8	CC423224 PUPF26TB
24	210.8	13.5	737	9	CG738302 ZMABH003

25	210.8	13.5	918	9	CG084733 PUKDU01TD
26	209.6	13.4	647	9	CG707522 1119002G0
27	209.2	13.4	886	9	CM002179 ZMABH000
28	208.6	13.3	837	8	CC338512 OGBG42TH
29	208.4	13.3	780	8	BZ988125 PUGB60TB
30	208.2	13.3	704	8	BZ796630 PUGBK90TD
31	207.8	13.3	1040	9	CL988912 ZMABH000
32	207.8	13.3	1085	9	CL990459 ZMABH000
33	206.8	13.2	761	8	BZ755899 PUPCG4TB
34	206.4	13.2	776	8	CC356868 PUDH62TD
35	206.4	13.2	919	8	CC426863 PDKC30TB
36	206.2	13.2	830	8	BZ796628 PUGBK90TD
37	206.2	13.2	973	8	CL994908 ZMABH000
38	205.2	13.1	998	8	CC383150 PUDH052TD
39	205.6	13.1	640	8	BZ804749 PUGB647TD
40	205.2	13.1	714	9	CM013617 ZMABH000
41	205.2	13.1	777	9	CG356927 OGBA20TV
42	205.2	13.1	778	9	CG356921 OGBA20TH
43	205.2	13.1	786	9	CG175670 PULB135TD
44	205.2	13.1	801	9	CM015229 ZMABH000
45	205.2	13.1	821	8	CC010502 PUBDA07TD

ALIGNMENTS

RESULT 1
CG005206/c
LOCUS ZUAE955TH ZM 3.0 4.0 KB Zea mays genomic clone ZMABPa0041022,
DEFINITION genomic survey sequence.
ACCESSION CG005206
VERSION CG005206.1 GI:33876322
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

AUTHORS Whitehead, C.A., Quackenbush, J., Van Aken, S., Uteerback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
1 (bases 1 to 776)

TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other GSSs: ZUAE955TV
Contact: Cathy Whitelaw

FEATURES

TIQR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES

Location/Qualifiers
1..776
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBA0041022"
/clone_1lb="ZM_3.0 4.0 KB"
/note="Vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered' genomic DNA library"

ORIGIN

Query Match 14.2% Score 222; DB 9; Length 776;
Best Local Similarity 79.3% Pred. No. 4.2e-41;
Matches 303; Conservative 0; Mismatches 70; Indels 9; Gaps 3;
C 214 GGCCTTACATCATCATCATCATCATCTTCGCGTGTCTCTTAAAGATTCATCTT 273
D 635 GTCTCTATATCATCTCTATATCGTCTTACAGTCTTCTTAAAGATTCATCTT 576

QY 274 CTGAATCTTATTCCTCCAAATAGGTTCTTAATCAGGTCCTAATA--GCATACCT 331
 DB 575 CTATATCTCTTCTCTCCACACAGCTCCTTAATACTCCTCTATACTCAATATCT 516
 QY 332 ATATTAGACAT-----TTTTATTTTTTTTGTACATACATATTGTCTACTCTCAAT 385
 DB 515 ATATTAGACATTTTTTATTTTTTATTTTTTTGTACATAGATATTCGCCGATCTCAAT 456
 QY 386 GCATTATACATA-TTTAGTTTACTAAACCGATTATTAAAGTATTCAAACGATGAAGA 444
 DB 455 GATATGTACATATTATTTAGTTTGTCTAAACCGTTATTAAAGTATTCAAATGATGAG 396
 QY 445 ACCTGTAGTAATCTATATATATAGAGATCCAGTACGCTCTTAATTTAGATGATT 504
 DB 395 ACCGTTAGAGAACTCTATACATAGAAATCCAGACGCTCTTAATTTAGAGACC 336
 QY 505 ATTTAGAGACGCTGTAGAAAACGTAAATAATCTTTGATTATTTATTTAGGGTAGA 564
 DB 335 GTTTAGAGGACGCTGTGAGGCGGTAGATGACCATTTGATCTCTATATTAGGGTAGA 276
 QY 565 GTTAGCCTTTATGCTTTATAGAT 586
 DB 275 GAACCTTTAGGGTTCTTGTCT 254

RESULT 2
 CC001894 293 bp DNA linear GSS 31-MAR-2003
 LOCUS PUEB307D ZM 0.6 1.0 KB Zea mays genomic clone ZMMB1A196B11,
 DEFINITION genomic survey sequence.
 ACCESSION CC001894
 VERSION CC001894.1 GI:29380454
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 293)
 WhiteIaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Benetzen,J.
 Maize Genomics Consortium
 Unpublished (2003)
 CONTACT: Cathy WhiteIaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteIaw@tigr.org
 Seq primer: TF
 Class: sheared ends.
 Location/Qualifiers
 1..293
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMB1A196B11"
 /clone_lib="ZM 0.6 1.0 KB"
 /note="Vector: pCR4-T0B0, Site 1: EcoRI, 0.6-1.0 kb high
 Cot selected genomic DNA library"

ORIGIN
 Query Match 14.1%; Score 221.2; DB 8; Length 293;
 Best Local Similarity 89.7%; Pred. No. 5,7e-41;
 Matches 278; Conservative 0; Mismatches 13; Indels 19; Gaps 3;

QY 610 CGGTATTTTGGGATTCGCTCTCTCACTTTCACTCCAGCG--CCCAATTTTACGTT 667
 DB 1 CGGTATTTTGGGATTCGCTCTCTCACTTTCACTCCAGCGCGCCCTCTTTTCAAGTT 60

QY 668 TTCACGGAAGCCCGAGCTGCTTAACCAAAATTTGATACGTCGCGGTTTTCAAAA 727
 DB 61 TTCACGGAAGCCCA-----GCCAAACCAAAATTTGATACGTCGCGGTTTTCAAAA 116
 QY 728 GAATCGGAACCATCTGACCCACCGACTAGTAGGCTCTGGATCTCTCGATTAACT 787
 DB 117 GAAGCCGGAACCATCTGACCCACCGACTAGTAGGCTCTGGATCTCTCGATTAACT 176
 QY 788 CCTAGCAATAGGAGCCGAGAACCGACATACGCGGATTCGCTTAGCTTCCACTCA 847
 DB 177 CTTAGCCAAATAGGAGCCGAGAACCGACATACGCGGATTCGCTTAGCTTCCACTCA 236
 QY 848 TCGGCGCGCTCATCTCCATCCACACCTATTCCCTTATCCCTGACCATCTCCGAAAAA 907
 DB 237 TCGGCGCGCTCATCTCCATCCACACCTATTCCCAAAATA-----CCATCTCCGAAAAA 283
 QY 908 TTCTCGGCTC 917
 DB 284 TTCTCGGCTC 293

RESULT 3
 BZ791049 853 bp DNA linear GSS 17-MAR-2003
 LOCUS PUFED01TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMB1A311B02,
 DEFINITION genomic survey sequence.
 ACCESSION BZ791049
 VERSION BZ791049.1 GI:28987056
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 853)
 WhiteIaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Benetzen,J.
 Maize Genomics Consortium
 Unpublished (2003)
 CONTACT: Cathy WhiteIaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteIaw@tigr.org
 Seq primer: TR
 Class: sheared ends.
 Location/Qualifiers
 1..853
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMB1A311B02"
 /clone_lib="ZM 0.6 1.0 KB"
 /note="Vector: pCR4-T0B0, Site 1: EcoRI, 0.6-1.0 kb high
 Cot selected genomic DNA library"

ORIGIN
 Query Match 14.0%; Score 218.8; DB 8; Length 853;
 Best Local Similarity 79.7%; Pred. No. 2.4e-40;
 Matches 298; Conservative 0; Mismatches 67; Indels 9; Gaps 3;

QY 214 GGCCTTACATCATCATATATATCATCTTTCGCTGCTCTTAAGATTCATCT 273
 DB 33 GTCCTTATATCATCTCTATATATCGTCTTTACAGTATATCTTAAAGATTTATCT 92
 QY 274 CTGAATCTTATTCCTCTCCAAATAGGTTCTTAAATCAGTCTCTATAA--GCATACCT 331
 DB 93 CTATATCTCTTCTCTCCACACAGTCTCTTAATTCAGTCTCTATATCTCAAAATATCT 152

QY	332	ATATTAGAGACAT-----TTTTATTTTTTGTACATACATTTGTCACTCTCAAT	385
Db	153	ATATTAGAGACATTTTTTATTTTATTTTATTTTGTACATACGATTTTGTATACTCTCAAT	212
QY	386	GCATTATACATA-TTTCAGTTTTTACTAAACCGATTTATTTTAAAGTATTCAAACGAGTAGA	444
Db	213	GTATTGTACATATTTTATTTTGTCTAAACCGGTATTTTAAAGTATTCAAAGTAAAGG	272
QY	445	ACTGTTTATGATTAATTTCTATATATATAGAAATCCAGTAGCGTCTCTAATTTAGATGATT	504
Db	273	ACCGTTTAGAGAACTCTATATATATATAGAAATCCAGCGTCTCTAATTTTAGAGACC	332
QY	505	ATTTAGAGAGCGCTGTAGAAAACGTAAAAAATTCCTTGATTTATTTATTTAGGGTAGA	564
Db	333	GTTTAGAGAGCGCTCTGAGAGCATAGAAATCATTTGATTCCTTATATTATTTAGGGTAGA	392
QY	565	GTAGCCTTATGCT	578
Db	393	GAACCTTTAGGCT	406

RESULT 4	BZ808218	864 bp	DNA	linear	GSS 17-MAR-2003
LOCUS	BZ808218				
DEFINITION	BZ808218	PUGGCC02TB ZM.0.6.1.0 KB zea mays genomic clone ZMMBT311B03,			
ACCESSION	BZ808218	Genomic survey sequence.			
VERSION	BZ808218.1	GI:29020571			
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	Whitelaw C.A., Quackenbush, J., Van Aken, S., Uterback, T., Renick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennerzen, J.				
TITLE	Maize Genomics Consortium				
JOURNAL	Unpublished (2003)				
COMMENT	Other_GSSs: PUGGC02TD				

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteplaw@tigr.org
Seq primer: TR
Class: sheared ends.

```

FEATURES
    source
        location/Qualifiers
            1. .864
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
                /db_xref="taxon:4577"
                /clone="ZMMB7A311B03"
                /clone_1lb="2M_0.6_1.0_KB"
                /note="Vector: pCR4::TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                    Cot selected genomic DNA library"

```

Query Match	14.0%;	Score 218.8;	DB 8;	Length 864;
Best Local Similarity	79.7%;	Pred. NO. 2.4e-40;		
Matches 288; Conservative	0;	Mismatches 67;	Indels 9;	Gaps 3;

QY	214	GGCCCTACATCATCACTATATATCAATCCTTTCGAGTGCTCTAAAGAATTCATCCT	273
Db	38	GGCCCTATATTCATCTCTATATCCGCTTTTACAGTAACTCTAAAGAATTTATCT	97
QY	274	CTGAATCTTATTCCTTCGATACGTTCTCTAAATCAAGTCTCTATA--GCATYACT	331
Db	98	CTATATTCCTTTCTCTCCAAACAAAGTCTCTAAATCAAGTCTCTATATCTCAATATCT	157

Oy	ATATTGAGACAT-----TTTTATTTTTTGACATCATATTTGTCATACCTCAAT	385
Oy	332 ATATTGAGACAT-----TTTTATTTTTTGACATCATATTTGTCATACCTCAAT	385
Db	158 ATATTGAGACATTTTTTATTTTTTATTTTTTTTGACATACGATTTTGTATATACCTCAAT	217
Oy	386 GCATTTATACATA-TTTAGTTTACTTAAACCGATTATTTAAAGTATCAAACGATGAGA	444
Db	218 GTATTGTACATATTTAGTTTGTCTAAACCGGTATTTTAAAGTATCAAACGATGAGA	277
Oy	445 ACAGTTAGTAAATCTATATATATAGAGATCCAGTAGCCGTTCTCTAAATTTAGATATT	504
Db	278 ACCGTTTAGAGAACTCTATATATAGAGATCCAGTAGCCGTTCTCTAAATTTAGAGACC	337
Oy	505 ATTTAAGAGACGCTGTTAGAAAACGTAAAAAATCTTGATTAATTTATATTTAGGATAGA	564
Db	338 GTTTAAGAGACGCTGCTGAGAGAGCATAGAGATCATTTGATCTCTATATATTTAGGGTACA	397
Oy	565 GTAGCCCTTATGCT 578	
Db	398 GAACCCCTTAGGGT 411	

RESULT	5
COSID	ZUAEM6790
LOCUS	
DEFINITION	CG018790 838 bp DNA linear GSS_19-AUG-2003 ZUAEM67H ZM.3.0.4.0 KB Zea mays genomic clone ZMMBPa0043L11, genomic survey sequence.
ACCESSION	CG018790
VERSION	CG018790.1 GI:33890955
KEYWORDS	GSS. Zeas mayas Zea mays
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euxariata; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 838)
REFERENCE	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Rendick,A., Fraser,C.M., Budiman,M.B., Bedell,J.B., Rohlfing,T., Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.
AUTHORS	Consortium for Maize Genomics
TITLE	Unpublished (2002)
JOURNAL	
COMMENT	Other_GSSs: ZUAEM66TV

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

```

FEATURES
    source
        location/Qualifiers
            1..838
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
                /db_xref="taxon:4577"
                /clone="ZMMBPa0043L1.1"
                /clone_lib="ZM 3.0 4.0 KB"
                /note="vector: pBSCsk-; Site_1: HincII; 3-4 kb 'unfiltered'
                genomic DNA library"

```

Query Match	14.0%	Score 218.4	DB 9	Length 838
Best Local Similarity	80.4%	Pred. No. 3e-40		
Matches 307	Conservative	0	Mismatches 66	Indels 9
				Gaps 4

Qy	214	GGCCCTTCAACATCAATCATATATTCATATCCCTTTCGGGTGTCCTTAAAGAATTCATCT	273
Db	6	GTCTCTATATATCAATCCGTATATCCGTACTTTACAGTCTCTCTAAAGAATTCATCT	65
Qy	274	CTGAATCTATATCTCTCCCATATACGTTCTCTAAATCAAGT-CCTCTTAAGC-AATACCT	331
Db	66	CTATATCTCATTTCTCTCCCAACAAGTCCTCTTAATACAGTACTTATCTCAAAATTCCT	125

OY		332	ATATTAGACAACTTTTETTA-----TTTTTGTCATCATATTTGTCATCTGCCAAT	385
OY		126	ATATTAGACAACTTTTATTTTGTGGTTTATATACATCGTATTTGTCTCAAT	185
OY		386	GCAATTATACATA-TTTAGTTTTACTAAACCGATATATTTAAAGTATTCAAACGATGAAGA	444
DB		186	GTATTATACATATTTTGGTTTGTGTAACC GGTTATTTAAAGTATTCAAATGGATAGAGG	245
OY		445	ACTGTTTGATTAATTTCTATATATATAGAAATCCAGTACCGTCTCTTAATTTTAGTATTT	504
DB		246	ACCGTTTGAGAAAACCTCATATGATAGAAATCCAGCACGCCTCTTAATTTTAGAGGACC	305
OY		545	AATTAGAGACGCGCTTGTAAGAAACGTAAAAATCTTTGATTTATTTAATTAGGATGA	564
DB		306	GTTTAGAGACGCGCTGAGACGACVAGAGACCAATTTGTCCTTATATTTAGGGTACA	365
OY		565	GTAGCCTTTATGCTTTATAGAT	586
DB		366	GAACCCCTTtaggctgtccttgcct	387
RESULT 6				
LOCUS		CL998388	1008 bp	DNA linear GSS 23-SEP-2004
DEFINITION		ZMMBHf01ln01.f ZMMBHf Zea mays genomic clone ZMMBHf01ln01 5'		
ACCESSION		CL998388		
VERSION		CL998388.1	GI:52570043	
KEYWORDS		GSS.		
SOURCE				
ORGANISM		Zea mays		
REFERENCE		Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.		
AUTHORS		Ma,J., SamMiguel,P., Liu,R., Haller,K., Soderlund,C. and Bennezen,J.		
TITLE		ZMMBH sequences		
JOURNAL		Unpublished (2004)		
COMMENT		Contact: Jeff Bennezen Bennezen Lab The University of Georgia Department of Genetics, C466 Life Sciences Building, Athens, GA 30602, USA Tel: 706-542-3698 Fax: 706-583-0972 Email: maize@uga.edu Plate: 0011 row: n column: 01 Class: BAC ends.		
FEATURES				
source		Location/Qualifiers		
		1..1008		
		/organism="Zea mays"		
		/mol_type="genomic DNA"		
		/culivar="B73"		
		/db_xref="taxon:4577"		
		/clone="ZMMBHf01ln01"		
		/tissue_type="immature ear"		
		/dev_stage="6-8 weeks"		
		/lab_host="DH10B"		
		/clone_id="ZMMBHf"		
		/note="Vector: TOPOcr4; Site_1: EcoRI; Site_2: EcoRI"		
ORIGIN				
Query Match		13.9%; Score 218; DB 9; Length 1008;		
Best Local Similarity		78.7%; Pred. No. 3.8e-40;		
Matches		Conservative 0; Mismatches 75; Indels 2; Gaps 2;		
OY		214	GCGCTTAACATCATCATATATATCATCTCTTCGCGTCTCTTAAGATTCATCT	273
DB		264	GGCTCTATATCATATATCATATATCGGCTTACATCATCTTAAGATTTATCTCT	323
OY		274	CTGATCTTATCTCTCCAAATAAGCTTCTCAATTCAGTCTCTATAAGC-AAATACCTA	332

Db	324	CTATATATTTCCCTCCCTCCAAACAAGTTCCTAATATCAGCTCCCTAATATGCAATATATCTA	383
Qy	333	TATTAGACATTTTTTATTTTTTTGGACATACATATTGGCATACCTGCAATGCAATAT	392
Db	384	TATTAGAGATTTTTTTTAAATTTTTTGTATATACGATTTATCATCTCTCAAAATGTAATGT	443
Qy	393	ACATA-TTTAGTTTACTAAACCGATTATTTTAAAGTATTCAAAACGATGAAGAACTGGTT	451
Db	444	ACATATTTTAGTTTGTCTAAACCAAGTTATTTTAAAGTATTCAAAATGGATAGATGGCGCTT	503
Qy	452	AGTAAATCTATATATAGAAATCCAGTACGTTCTCTAAATTTTGAATGATTATTAGA	511
Db	504	AAAAAACTCTATATATAGAGATCCAGCAAGTTCTCTAAATTTTAGAGAACCGTTTAGA	563
Qy	512	GGACGCTGTTAGAAAACGTAAAAAATTCCTTGATTATTTATTTTGAAGTAGAGTACCT	571
Db	564	GGACATCTGTTAAAGCGGTAGAGACCGATTAAACCTATATATTAGAGTAGACGAAGGCT	623
Qy	572	TT 573	
Db	624	TT 625	

RESULT 7	
LOCUS	CL998109
DEFINITION	CL998109 1026 bp DNA linear GSS 23-SEP-2004 ZMMBHf0011h03.f ZMMBHf Zea mays genomic clone ZMMBHf0011h03 5', genomic survey sequence.
ACCESSION	CL998109
VERSION	CL998109.1 GI:52569489
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays

REFERENCE	1 (bases 1 to 1008)
AUTHORS	Ma,J., Sammiquel,P., Liu,R., Haller,K., Soderlund,C. and Bennett,J.
TITLE	ZMBH sequences
JOURNAL	Unpublished (2004)
COMMENT	Contact: Jeff Bennett

JOURNAL
COMMENT
Unpublished (2004)
Contact: Jeff Bennetzen
Bennetzen Lab
The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, GA
30602, USA
Tel: 706-542-3698
Fax: 706-583-0972
Email: maize@uga.edu
Plate: 0011 row: n column: 01
Class: BAC ends.
Location/Qualifiers
1..1008

FEATURES	SOURCE	Location/Qualifiers
		1..1008
		/organism="Zea mays"
		/mol_type="genomic DNA"
		/cultivar="B73"
		/db_xref="taxon:4577"
		/clone="ZMMBHf0011n01"
		/tissue_type="Immature ear"
		/dev_stage="6-8 weeks"
		/lab_host="DH10B"
		/clone_1b="ZMMBHf"
		/note="Vector: TOPopcr4; Site_1: EcoRI; Site_2: EcoRI"

Query Match	13.9%	Score 218	DB 9	Length 1008
Best Local Similarity	78.7%	Pred. No. 3.8e-40		
Matches 285	Conservative	0	Mismatches 75	Indels 2
				Gaps 2

QY 214 GGGCTTACATCATCATATATATCATCATCTTCCGGGAGTCCCTAAAGAATTCATCCT 273

Db 264 GTCCCTATATTCATATATATATATATCGTCTTTACATATCTATTAAGAATTTATCCT 323

QY 274 CTGAATCTTATTCCTCCATATAGGTTCTTAATCAGGTCTCATAGC -AATACCTA 332

Db	324	CTATATATTTCCCTCCCTCCAAACAAGTTCCTAATATCAGCTCCCTAATATGCAATATATCTA	383
Qy	333	TATTAGACATTTTTTATTTTTTTGGACATACATATTGGACATCTGCAATGACATTTAT	392
Db	384	TATTAGAGATTTTTTTTAAATTTTTTGTATATACGATTTATCATCTCTCAAAATGTAATGT	443
Qy	393	ACATA-TTTAGTTTACTAAACCGATTATTTTAAAGTATTCAAAACGATGAAGAACTGGTT	451
Db	444	ACATATTTTAGTTTGTCTAAACCAAGTTATTTTAAAGTATTCAAAATGGATAGATGGCGCTT	503
Qy	452	AGTAAATCTATATATAGAAATCCAGTACGTTCTCTAAATTTTGAATGATTAATTAGA	511
Db	504	AAAAAACTCTATATATAGAGATCCAGCAGATTCCTAAATTTTAGAGAACCGTTTAGA	563
Qy	512	GGACGCTGTGTAAGAAACGTAAAAAATTCCTTGATTATTTATTTTGAAGTAGAGTACCT	571
Db	564	GGACATCTGTAAAGACGCGTAGAGGACCGATTAAACCTATATTTAGAGTAGACGAAGGCT	623
Qy	572	TT 573	
Db	624	TT 625	

RESULT 7	
LOCUS	CL998109
DEFINITION	CL998109 1026 bp DNA linear GSS 23-SEP-2004 ZMMBHf0011h03.f ZMMBHf Zea mays genomic clone ZMMBHf0011h03 5', genomic survey sequence.
ACCESSION	CL998109
VERSION	CL998109.1 GI:52569489
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays

REFERENCE
AUTHORS
TITLE
ZMBH sequences

TITLE	JOURNAL	COMMENT
Bennetzen, J.	ZMMBH sequences Unpublished (2004)	
Contact: Jeff Bennetzen		
Bennetzen Lab		
The University of Georgia		
Department of Genetics, C426a Life Sciences Building, Athens, GA		
30602, USA		
Tel: 706-542-3698		
Fax: 706-583-0972		
Email: maize@uga.edu		
Plate: 0011 row: h column: 03		
Class: BAC ends.		

FEATURES	Plate: 0011	row: h	column: 03
source	Class: BAC ends.		
	Location/Qualifiers		
	1..1026		
	/organism="Zea mays"		
	/mol_type="genomic DNA"		
	/cul_tivar="B73"		
	/db_xref="taxon:4577"		
	/clone="ZMMBHFD001h03"		
	/tissue_type="Immature ear"		
	/dev_stage="6-8 weeks"		
	/lab_host="DH10B"		
	/clone_11b="ZMMBHf"		

Query Match: 13.9%; Score 218; DB 9; Length 1026;

[illegible]

OY	274	CTGAATCTATTCCCTCCCAATAAGCTCTCTAAATCAAGGCTCTATAAGC-AATACCTA	332
Db	324	CTATTATCTTGGCCCTCCCAACAAAGTCTCTAAATCAAGTCCCTATATGAAAAATCTA	383
OY	333	TATTAGAGACATTTTATTTTTTTGTACATACATTTGTCACTCTCAAAATGCAATAT	392
Db	384	TATTAGAGATTTTTTATTTTTTTGTATATAGCAATTAATCAATCTCAAAATGATATGT	443
OY	393	ACATA-TTTAGTTTACTAAACCGATTTATTTAAATATTTCAACGATGAAGATCTGTT	451
Db	444	ACATATTTTAGTTTGTCTAAACCAAGTATTTTAAAGATATTCAAATGATAGTGGCCGCTT	503
OY	452	AGATTAATCTATATATATAGAGATCCAGTAGCGTCTCTAAATTTAGATGATTATTAGA	511
Db	504	AAAAAATCTATATATATAGAGATCCACAGAGTCTCTAAATTTAGAGAACCGTTTGA	563
OY	512	GGAGCGCTGTAGAAAAAGTAAAAAATCTTGATTAATTATATTTAGGGTGAAGTAGCTT	571
Db	564	GGACACTCTCTAAAGAGCGTAGAGACCAATTAACCTCTATATTTAGAGTACAGAAAGCT	623
OY	572	TT 573	
Db	624	TT 625	

[illegible][illegible]

RESULT 9	CD437683	CD437683	861 bp	mRNA	linear	EST 03-JUN-2003
LOCUS	CD437683					
DEFINITION	EL01N0503H03.1	b	EndospERM_5	Zea mays	cdna	mRNA sequence.
ACCESSION	CD437683					
VERSION	CD437683.1		GI:3153326			
KEYWORDS	EST.					
SOURCE	Zea mays					
ORGANISM	Zea mays					

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACAD clade; Panicoideae; Andropogoneae; Zea.	1 (bases 1 to 795)			
	Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkin, B., Becraft, P. and Messing, J.	Characterization of the maize endosperm transcriptome and its comparison to the rice genome	Genome Res. 14 (10), 1932-1937 (2004)	
	Contact: Lai, Jinhsheng			
	Dr. Joachim Messing's lab			
	Wakeman Institute, Rutgers University			
	190 Frelinghuysen Rd., Piscataway, NJ 08854, USA			
	Tel. 732-445-3801			
	Fax: 732-445-5735			
	Email: jlai@wakeman.rutgers.edu			
	Seq primer: 73.			

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 861)
Lai,J., Day,N., Kim,C.S., Bharti,A.K., Rudd,S., Mayer,K.F.,
Larkin,B., Becraft,P. and Messing,J.
Characterization of the maize endosperm transcriptome and its
comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel.: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: 13.

FEATURES	Location/Qualifiers
source	1. .795

FEATURES	Location/Qualifiers
source	1. .861

```

/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W2"
/db_xref="taxon:4577"
/risue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_5"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

```

```

/cultivar="M21"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_5"
/note="Vector: pBluescript SK-, Site_1: EcoRI, Site_2:
XhoI"

```

ORIGIN

ORIGIN

	Query Match	13.9%	Score 217.2	DB 6	Length 795
	Best Local Similarity	78.5%	Pred. No. 5.7e-40		
	Matches	300	Conservative	0	Mismatches 73; Indels 9; Gaps 3;
QY	214	GACCTTAACATCATCATATATATCATCTTCGCGTGCCTCTAAAGAATTCATCCT	273		
DB	324	GGCCCTATATTCATCTCTATATTCGCTTTTAAAGTCTCCTCTAAAGAATTCATCTCT	383		
QY	274	CTGAATCTTATTCCTCTCCAAATACGTTCTCTAAATGAGGTCTTATTA--GCATATACCT	331		

Query Match	Similarity	13.9%	Score 217.2	DB 6	Length 861
Best Local	Similarity	78.5%	Pred. No. 5.7e-40		
Matches	300	Conservative	0	Mismatches	73
				Indels	9
				Gaps	3
Qy	214	GGCCTTCAACATTCACATCTTAATATTCATCCCTTCGCGTCTCTTAAAGATTGCATCTCT	273		
Db	383	GTCCTCAATATTCACATCCCTCTTAATATTCATCCCTCTTAAAGATTGCATCTCT	442		
Qy	274	CTGATCTTATATCTCTCTCCACATAACGTTCTCTTAATACGGTCTCTATATA--GGATATACCT	331		
Db	443	CTTATATCTCTCTCTCTCTCCAAACAGCGCTCTTAATACAGCTCTCTTATCTCAAAATTCCT	502		

QY 332 ATATTAGACAT-----TTTTATTTTGTAGACATATTTGTCTCAAT 385
 |||||
 Db 503 AATATTAGAAACATTTTATTTTATTTTGTAGACATATTTGTCTCAAT 562
 |||||
 QY 386 GCATTATACATA-TTTAGTTTACTTAACCGATTATTAAAGTATTCAAACGATGAAGA 444
 |||||
 Db 563 GATATTGTATATATTATTAGTTTGTCTTAACACGATTATTAAAGTATTCAAATGATGAGG 622
 |||||
 QY 445 ACCTGTAGTAATCTATATATTAGAGATCCAGTAGGCTCTAAATTTAGATGATT 504
 |||||
 Db 623 ACCGTTTAGAGAACTCTATATATTAAGATTCAGACGCAATCTTAATTTAGAGAACT 682
 |||||
 QY 505 ATTAGAGACAGCTGTAGAAAACGTAAATAATCTTGTATTTATATTAGAGGTAGA 564
 |||||
 Db 683 GTTTAAGAGACGCTGTGAGAGGCGTAGAGTACATTGATCTCTATATTTAGGTTACA 742
 |||||
 QY 565 GTAGCCTTTATGCTTTATATAGAT 586
 |||||
 Db 743 GAACCTTTAGGCTCTTGCT 764

RESULT 10
 CL988337 988 bp DNA linear GSS 23-SEP-2004
 LOCUS ZMBHe005f06.r ZMBHe Zea mays genomic clone ZMBHe005f06 3',
 DEFINITION genomic survey sequence.
 ACCESSION CL988337
 VERSION CL988337.1 GI:52556415
 KEYWORDS GSS.

SOURCE

ORGANISM Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 988)
 Ma,J., Sanlignel,P., Liu,R., Haller,K., Soderlund,C. and
 Bennetzen,J.

REFERENCE

TITLE ZMBH sequences
 JOURNAL Unpublished (2004)
 COMMENT Contact: Jeff Bennetzen
 Bennetzen Lab
 The University of Georgia
 Department of Genetics, C426a Life Sciences Building, Athens, GA
 30602, USA
 Tel: 706-542-3698
 Fax: 706-583-0972
 Email: maize@uga.edu
 Plate: 0005 Row: f column: 06
 Class: BAC ends.

FEATURES

source 1..988
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /culivar="B73"
 /db_xref="taxon:4577"
 /clone="ZMBHe005f06"
 /tissue_type="immature ear"
 /dev_stage="6-8 weeks"
 /lab_host="DH10B"
 /clone_lib="ZMBHe"
 /note="Vector: TOPOpcr4; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Query Match 13.8%; Score 216.4; DB 9; Length 988;
 Best Local Similarity 78.5%; Pred. No. 9e-40;
 Matches 284; Conservative 0; Mismatches 76; Indels 2; Gaps 2;
 214 GGCCCTAACATCATCATATATATCATCTTCCGCTGCTCTTAAAGATCCATCTT 273
 |||||
 Db 264 GTCTCTATGTTATATATATATATCCGCTCTTACATCTACTTAAAGATTTTATCT 323
 |||||
 QY 274 CTGAATCTTATTCCTCTCAATAACGTTCTCTAATCAGGTTCTTATAGC-AATACTTA 332
 |||||

Db 324 CTATATATCTTGCTCTCCCAACAGCTTCTTAAATCAGTCCCTATATGCAATATCTTA 383
 |||||
 QY 333 TATTAGACATTTTATTTTATTTTGTAGACATATTTGTCTCAATCTCAATGATTAT 392
 |||||
 Db 384 TATTAGAGATTTTATTTTATTTTGTATATAGCATTTATCATCTCAATATGATTCGT 443
 |||||
 QY 393 ACATA-TTTAGTTTACTTAACCGATTATTTAAAGTATTCAAACGATGAGAACTGTTT 451
 |||||
 Db 444 ACATATTTAGTTTGTCTTAACCACTTATTTTAAATGATTCAAATGATGATGCGGCTT 503
 |||||
 QY 452 ACATATATCTTATATATAGAAATCCAGTAGGCTCTCAATTTAGATGATTATTTGA 511
 |||||
 Db 504 AAAAAAAGCTTATATATAGAGATCCACAGAGTTCTCAATTTTAGAGAACCGTTTGA 563
 |||||
 QY 512 GGACGCTGTAGAAACGTAAATAATCTTGTATTTATTTATTTAGGTTAGTAGAGCT 571
 |||||
 Db 564 GGACACTGCTTAAGAGCGTAGAGACCGATTAACTCTATATTTTAGATACAGAAAGCT 623
 |||||
 QY 572 TT 573
 ||
 Db 624 TT 625

RESULT 11
 CG152598 807 bp DNA linear GSS 21-AUG-2003
 LOCUS PUIH317D ZM 0.6 1.0 KB Zea mays genomic clone ZMBHe0609E14,
 DEFINITION genomic survey sequence.
 ACCESSION CG152598
 VERSION CG152598.1 GI:34043393
 KEYWORDS GSS.

SOURCE

ORGANISM Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 807)
 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uteckack,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguell,P., Ma,J. and
 Bennetzen,J.

REFERENCE

TITLE Maize Genomics Consortium
 JOURNAL Unpublished (2003)
 COMMENT Other GSSs: PUIH317B
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TF
 Class: sheared ends.

FEATURES

source 1..807
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMBHe0609E14"
 /clone_lib="ZM_0.6 1.0 KB"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
 Cor selected genomic DNA library"

ORIGIN

Query Match 13.8%; Score 216.2; DB 9; Length 807;
 Best Local Similarity 79.4%; Pred. No. 9.8e-40;
 Matches 296; Conservative 0; Mismatches 68; Indels 9; Gaps 3;
 223 ATCCATCATCTATATATCATCTTTCGCTGCTCTTAAAGATTCATCTGATCTT 282
 |||||
 Db 330 ATCCATCATCTATATATCATCTTTCACGCTCATCTTAAAGATTTATCTCTATATTC 389
 |||||
 QY 283 ATTCTCTCAATAACGTTTCTTAAATCAGGTTCTATTA--GCAATACCTATTTAGAG 340
 |||||

Db 390 CTCCTCCCAACAAGCTCTTAATTAAGCTTCTATACGAAATACCTATATTAG 449
 QY 341 ACAT-----TTTTATTTTGTGACATACATATTGTCTACTCTAAATGCATTATAC 394
 Db 450 ACATTTTATTTTATTTTATTTTGTGACATATGATATTTCTCACTCACTCAAAATGATTTATAC 509
 QY 395 ATA-TTTAGTTTACTAAACGATTTATTTAAGATTCAACGATGAAGAACGCTTAG 453
 Db 510 ATATTGTAGTTTGTCTAAACCGGTTATTATTAAGATTCAAAATGAGATAGAGACCGTTTAC 569
 QY 454 ATAAATCTATATATAGAGATCCAGTAGCGTTCTCTAAATTTAGATGATTTATTAGAG 513
 Db 570 AGAACTCTATATATAGAGATTTAGACGGTACTCTAAATTTAGAGACCATTTAGAG 629
 QY 514 ACCGTGTAGAAAACGTAAAAAATCTTTGATTTATTTATTTAGGTTAGAGTACCTTT 573
 Db 630 ACCGTGTGTATAGCGTAGAGATCATTTGATCTCTATATTTAGAGTATGATGACCTTT 689
 QY 574 ATGCTTATAGAT 586
 Db 690 AGATTACTTGTCT 702

RESULT 12

LOCUS CM015128 728 bp DNA linear GSS 23-SEP-2004
 DEFINITION ZMMBLC0007E02.x ZMMBLC Zea mays genomic clone ZMMBLC0007E02 3',
 genomic survey sequence.
 ACCESSION CM015128
 VERSION CM015128.1 GI:52603464
 KEYWORDS GSS.

SOURCE

ORGANISM Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 728)

REFERENCE

AUTHORS Wing, R., Luo, M., Soderlund, C. and Haller, K.
 TITLE ZMMBL sequences
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: http://genome.arizona.edu
 Plate: 0007 row: E column: 02
 Class: BAC ends.

FEATURES

source

Location/Qualifiers
 1..728
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBLC0007E02"
 /issue_type="immature ears"
 /lab_host="DH10B T1 phage resistant"
 /clone_lib="ZMMBLC"
 /note="Vector: pAGIBAC1; Site_1: Hpa II; Site_2: Hpa II"

ORIGIN

Query Match 13.8%; Score 215.6; DB 9; Length 728;
 Best Local Similarity 78.3%; Pred. No. 1.3e-39;
 Matches 299; Conservative 0; Mismatches 74; Indels 9; Gaps 3;

QY 214 GGCCTTCAATCATCATATCATATCCCTTTCCGCTGCTCTAAAGATTCATCCT 273
 Db 165 GTCTCTATATATATATCTCTATATCCGCTCTTACAGCTCTCTAAAGATTTTATACCT 224
 QY 274 CTGAATCTTATTCCTCTCCAAATAGCTTCTCTAAATAGGCTCTATAA--GCAATACCT 331
 Db 225 CTATATCTCTCTCTCTCCAAACAGCTCTCTATATACAGCTCTCTATATCAAAATATCT 284

QY 332 ATATAGACAT-----TTTTATTTTGTGACATACATATTGTCTACTCTCAAT 385
 Db 285 ATATTGAAACATTTTATTTTATTTTGTGACATAGATTTGTCTACTCTCAAT 344
 QY 386 GCATATACATA-TTTAGTTTACTAAACCGATTTATTAAAGATTCAACGATGAGA 444
 Db 345 GTATTGTACATATTATTAGTTTGTCTAAACAGTATTTAAAGATTCAATGATGAG 404
 QY 445 ACTGTTAGATAATTTCTATATATAGAGATCCAGTAGCGTTCTCTAAATTTAGATGATT 504
 Db 405 ACCGTTAGAGAACTCTATACATAGAGATCCAGAGGTCCTCTAAATTTAGAGACC 464
 QY 505 ATTTAGAGACGCTGTAGAGAAAACGTAAAAAATCTTTGATTTATTTATTTAGGTTAGA 564
 Db 465 ATTTAGAGACGCTGTCTGAGAGCGGTAGAGACCATTTGTCTCTATATTTAGGGTTACA 524
 QY 565 GTAGCCTTATGCTTATAGAT 586
 Db 525 GAACCTTTAGGTTCTTGTCT 546

RESULT 13

LOCUS CG196646 874 bp DNA linear GSS 21-AUG-2003
 DEFINITION PUDBR84TB_ZM_0.6_1.0_KB Zea mays genomic clone ZMBRta0644N24,
 genomic survey sequence.
 ACCESSION CG196646
 VERSION CG196646.1 GI:34087707
 KEYWORDS GSS.

SOURCE

ORGANISM Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 874)

REFERENCE

AUTHORS White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
 Bennettzen, J.
 TITLE Maize Genomes Consortium
 JOURNAL Unpublished (2003)
 COMMENT Other GSSs: PUDBR84TD
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@cigr.org
 Seq primer: TR
 Class: sheared ends.

FEATURES

source

Location/Qualifiers
 1..874
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMBRta0644N24"
 /clone_lib="ZM 0.6_1.0 KB"
 /note="Vector: pCR4-TOPO; Site_1: BcoRI; 0.6-1.0 kb high
 cot selected genomic DNA library"

ORIGIN

Query Match 13.8%; Score 215.6; DB 9; Length 874;
 Best Local Similarity 78.3%; Pred. No. 1.4e-39;
 Matches 299; Conservative 0; Mismatches 74; Indels 9; Gaps 3;

QY 214 GGCCTTCAATCATCATATCATATCCCTTTCCGCTGCTCTAAAGATTCATCCT 273
 Db 204 GTCTCTATATATATATCTCTATATCCGCTCTTACAGTCTCTCTAAAGATTTATACCT 263
 QY 274 CTGAATCTTATTCCTCTCCAAATAGCTTCTCTAAATCAGGCTCTATAA--GCAATACCT 331
 Db 264 CTATATCTATTTCTCTCCAAACAGCTCTCTATATACAGTCTCTATATCTCAAAATATAT 323


```
QY 332 ATATTAGACATTTTAAATTT-----TTGTACATACATTTGTCACTCTCAAT 385
Db 567 ATATTAGACATTTTCTTATTTTAAATTTTACATACGATCTATCACTCTCAAT 626
QY 386 GCATTATACATA-TTTAGTTTACTAAACCGATTATTAAAGTATCAACGATGAAGA 444
Db 627 GTATTGTACATATTTTGTGTTTGTCTAAACCGTATTTAAAGTATTTAAATGGATAGAGA 686
QY 445 ACTGTTTAAATAATTTCTATATATATAGAAATCCAGTACGTTCTTAATTTAGATGATT 504
Db 687 ACCGTTTAAAGAACTCTATATATATAGAAATCCAGACGCTCTTAATTTAGAGAGACC 746
QY 505 ATTTAGAGACGCTGTAGAAACGTAAATAATCTTGAATATTTATTTAGGGTAGA 564
Db 747 GTTTGATTAACGCTGTGAAGAGCGTGAAGAGACCTTTGATCTCTAATTTAGGGTACA 806
QY 565 GTAGCCTTTATGCTTTATAGATCT 588
Db 807 GAACCTTTAGAGTCACTTGAGCT 830
```

Search completed: September 12, 2005, 03:55:43
Job time : 4113.12 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 00:10:11 ; Search time 220.914 Seconds
(without alignments)
11591.729 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565
Sequence: 1 GAATTCCTGAGGTGACGCG.....TTTTTGTAGTACGACG 1565

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1565	100.0	1565	4 US-09-037-531-3	Sequence 3, Appl1
2	1021	65.2	1021	4 US-09-037-531-1	Sequence 1, Appl1
3	454	29.0	454	4 US-09-037-531-2	Sequence 2, Appl1
4	428.8	27.4	1392	1 US-08-144-602B-6	Sequence 6, Appl1
5	428.8	27.4	1404	1 US-08-144-602B-7	Sequence 7, Appl1
6	428.8	27.4	2199	1 US-08-144-602B-5	Sequence 5, Appl1
7	428.8	27.4	5643	1 US-08-144-602B-4	Sequence 4, Appl1
8	426.2	27.2	623	3 US-09-078-862-5	Sequence 5, Appl1
9	378.4	24.2	4032	3 US-09-068-101-5	Sequence 5, Appl1
10	378.4	24.2	4032	4 US-09-970-921-5	Sequence 5, Appl1
11	375.8	24.0	3039	4 US-09-377-466B-19	Sequence 19, Appl1
12	375.8	24.0	3039	4 US-09-377-466B-21	Sequence 21, Appl1
13	375.8	24.0	3044	4 US-09-377-466B-38	Sequence 38, Appl1
14	375.8	24.0	3450	4 US-09-377-466B-17	Sequence 17, Appl1
15	375.8	24.0	3455	4 US-09-377-466B-36	Sequence 36, Appl1
16	375.8	24.0	3469	4 US-09-377-466B-23	Sequence 23, Appl1
17	358.8	22.9	2378	4 US-09-441-340-27	Sequence 27, Appl1
18	333.2	21.3	3694	3 US-09-080-625-5	Sequence 5, Appl1
19	333.2	21.3	3694	3 US-09-695-782-5	Sequence 5, Appl1
20	333.2	21.3	3877	3 US-09-080-625-4	Sequence 4, Appl1
21	333.2	21.3	3877	3 US-09-695-782-4	Sequence 4, Appl1
22	310.2	19.8	2107	3 US-09-441-340-29	Sequence 29, Appl1
23	310.2	19.8	2122	3 US-09-441-340-25	Sequence 25, Appl1
24	165.8	10.6	1084	3 US-08-604-789B-14	Sequence 14, Appl1
25	165.8	10.6	1084	3 US-09-312-721A-14	Sequence 14, Appl1
26	165.8	10.6	1084	4 US-09-733-300-14	Sequence 14, Appl1
27	77.4	4.9	7218	1 US-08-232-463-14	Sequence 14, Appl1

28	60	3.8	126176	4 US-09-949-016-16137	Sequence 16137, A
29	60	3.8	126176	4 US-09-949-016-16138	Sequence 16138, A
30	59.6	3.8	1141	4 US-09-806-708B-22	Sequence 22, Appl1
31	55.8	3.6	1055	4 US-09-806-708B-23	Sequence 23, Appl1
32	55.2	3.5	237241	4 US-09-949-016-16101	Sequence 16101, A
33	54.6	3.5	231129	4 US-09-949-016-16110	Sequence 16110, A
34	54.6	3.5	266293	4 US-09-949-016-11934	Sequence 11934, A
35	54.2	3.5	187169	4 US-09-949-016-12776	Sequence 12776, A
36	54.2	3.5	191569	4 US-09-949-016-15940	Sequence 15940, A
37	52.4	3.3	231129	4 US-09-949-016-16110	Sequence 16110, A
38	52.4	3.3	266293	4 US-09-949-016-11934	Sequence 11934, A
39	52	3.3	601	4 US-09-165-264-13	Sequence 15635, A
40	51.6	3.3	320	3 US-09-165-264-8	Sequence 8, Appl1
41	51.2	3.3	319	3 US-09-165-264-8	Sequence 12896, A
42	51.2	3.3	451924	4 US-09-949-016-12896	Sequence 17305, A
43	51.2	3.3	451925	4 US-09-949-016-17305	Sequence 12, Appl1
44	51	3.3	318	3 US-09-165-264-12	Sequence 7, Appl1
45	51	3.3	320	3 US-09-165-264-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-037-531-3
Sequence 3, Application US/09037531
Patent No. 6750378
GENERAL INFORMATION:
APPLICANT: Freysinet, Richard
TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037, 531
FILING DATE: 10-MAR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McMorrow Jr., Robert G.
REGISTRATION NUMBER: 30962
REFERENCE/DOCKET NUMBER: 5500*24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)658-9141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-037-531-3
Query Match 100.0%; Score 1565; DB 4; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCCTGAGGTGACGCGATCCCTATGTGACCATTTACTGTAAATGATATCAT 60
Db 1 GAATTCCTGAGGTGACGCGATCCCTATGTGACCATTTACTGTAAATGATATCAT 60

Query Match	65.2%;	Score 1021;	DB 4;	Length 1021;
Best Local Similarity	100.0%;	Pred. No. 1.2e-272;		
Matches 1021; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	27	CTTATGAGCACTTACTGTGATGATGCAATATCATTTATTTGAAATGCAAACTTTTCTAT	86
Db	1	CTTATGAGCACTTACTGTGATGATGCAATATCATTTATTTGAAATGCAAACTTTTCTAT	60
QY	87	ACTTCCTTACTTAACATTAATCTTGATTTTAAATTCAGTCTCTCAACATTCATGCTCAAG	146
Db	61	ACTTCCTTACTTAACATTAATCTTGATTTTAAATTCAGTCTCTCAACATTCATGCTCAAG	120
QY	147	TATATGTTGAGACGTGTCAAAATTTACATATTTTATTTCTTCATATTTTCTTCTATACA	206
Db	121	TATATGTTGAGACGTGTCAAAATTTACATATTTTATTTCTTCATATTTTCTTCTATACA	180
QY	207	CATTTTGGGCGCTTAACATCCATCCATCATATCCATCCCTTCCGGGTGCTCTAAAGAAAT	266
Db	181	CATTTTGGGCGCTTAACATCCATCATATCCATCCCTTCCGGGTGCTCTAAAGAAAT	240
QY	267	CCATCCTCTGATCTTATTCCTCTCAATAACGTTCTCTAAATCAGGTCTCTATTAAGCA	326
Db	241	CCATCCTCTGATCTTATTCCTCTCAATAACGTTCTCTAAATCAGGTCTCTATTAAGCA	300
QY	327	TACCTATATTTAGACATTTTATTTTATTTTGTACATACATATTTGTCTACTTCAATG	386
Db	301	TACCTATATTTAGACATTTTATTTTATTTTGTACATACATATTTGTCTACTTCAATG	360
QY	387	CATATATCATTTAGTTTATTTACTTAAACGATTAATTTAAAGTATTCAAACGATGAAGAC	446
Db	361	CATATATCATTTAGTTTATTTACTTAAACGATTAATTTAAAGTATTCAAACGATGAAGAC	420
QY	447	TGTTTAGATTAATTCATATATTAAGAAATCCAGTAGCGTTCTTAATTTAGATGATTAAT	506
Db	421	TGTTTAGATTAATTCATATATTAAGAAATCCAGTAGCGTTCTTAATTTAGATGATTAAT	480
QY	507	TTTAAAGACGCGTTTAABAAAACGTAAAAAATCTTGTGATTTTATATATTTAGGTAGAGT	566
Db	481	TTTAAAGACGCGTTTAABAAAACGTAAAAAATCTTGTGATTTTATATATTTAGGTAGAGT	540
QY	567	AGCCTTATGCTTATATAGATCTTTTGTGTGAGACCAAGCCTTATACGGTAAATTTGCGATTT	626
Db	541	AGCCTTATGCTTATATAGATCTTTTGTGTGAGACCAAGCCTTATACGGTAAATTTGCGATTT	600
QY	627	GCGCCTCTCATTTTCACTCCACGCGCCCAATTTACGTTTTCACGAGCGGCCACGC	686
Db	601	GCGCCTCTCATTTTCACTCCACGCGCCCAATTTTACGTTTTCACGAGCGGCCACGC	660
QY	687	TGCTTAACCAAAATTTGTATCGGTGGCGGGTTTTCAAAAGAAATCGAAAACCATCTGC	746
Db	661	TGCTTAACCAAAATTTGTATCGGTGGCGGGTTTTCAAAAGAAATCGAAAACCATCTGC	720
QY	747	ACCACACGACTAGTAGGCGCTCGGATCTCTCGTATTAATGCTTAGCAATATAGAGACCA	806
Db	721	ACCACACGACTAGTAGGCGCTCGGATCTCTCGTATTAATGCTTAGCAATATAGAGACCA	780
QY	807	GAACCACCCATCAGCGGAGTGTCTCTTAGCTTCCACTCATCGGCGCGTCTCATCTTCCA	866
Db	781	GAACCACCCATCAGCGGAGTGTCTCTTAGCTTCCACTCATCGGCGCGTCTCATCTTCCA	840
QY	867	TTCAAACACTATTCGTTACCTTACCTTGCCCATCTCTCGAAAATAATTCCTCGGCTGCGCTCCG	926
Db	841	TTCAAACACTATTCGTTACCTTACCTTACCTTCCGAAAATAATTCCTCGGCTGCGCTCCG	900
QY	927	ACCTACTACAAATTAACCATCCCATCAGACGCAATGCATCATCTGCAATATCCCCAGAA	986
Db	901	ACCTACTACAAATTAACCATCCCATCAGACGCAATGCATCATCTGCAATATCCCCAGAA	960
QY	987	ATCAACAACCTCCCAATTTCCACGCTGACCAACCAATGCGCTCTCTCGGCGCCAGACCCAA	1046
Db	961	ATCAACAACCTCCCAATTTCCACGCTGACCAACCAATGCGCTCTCTCGGCGCCAGACCCAA	1020

QY	1047	G	1047
Db	1021	G	1021

```

1      RESULT 3
2      US-09-037-531-2
3      / Sequence 2, Application US/09037531
4      / Patent No. 6750378
5      / GENERAL INFORMATION:
6      / APPLICANT: Derose, Richard
7      / APPLICANT: Freysinet, Georges
8      / TITLE OF INVENTION: Maize H3c4 Promoter Combined With The
9      / TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
10     / TITLE OF INVENTION: And Transformed Plant
11     / NUMBER OF SEQUENCES: 5
12     / CORRESPONDENCE ADDRESSES:
13     / ADDRESSEE: Connolly, Bove, Lodge, & Hutz
14     / STREET: 1220 Market Street
15     / CITY: Wilmington
16     / STATE: DE
17     / COUNTRY: USA
18     / ZIP: 19899
19     / COMPUTER READABLE FORM:
20     / MEDIUM TYPE: Floppy disk
21     / COMPUTER: IBM PC compatible
22     / OPERATING SYSTEM: PC-DOS/MS-DOS
23     / SOFTWARE: Patentln Release #1.0, Version #1.25
24     / CURRENT APPLICATION DATA:
25     / APPLICATION NUMBER: US/09/037,531
26     / FILING DATE: 10-MAR-1998
27     / CLASSIFICATION: 800
28     / ATTORNEY/AGENT INFORMATION:
29     / NAME: McMorrow Jr., Robert G.
30     / REGISTRATION NUMBER: 30962
31     / REFERENCE/DOCKET NUMBER: 5500+24
32     / TELECOMMUNICATION INFORMATION:
33     / TELEPHONE: (302)658-9141
34     / INFORMATION FOR SEQ ID NO: 2:
35     / SEQUENCE CHARACTERISTICS:
36     / LENGTH: 454 base pairs
37     / TYPE: nucleic acid
38     / STRANDEDNESS: single
39     / TOPOLOGY: linear
40     / MOLECULE TYPE: DNA (genomic)
41     / US-09-037-531-2

```

Query Match	29.0%	Score 454	DB 4	Length 454
-------------	-------	-----------	------	------------

Qy	1102	GTAAACACCCCGCCCTCCTCTCTTCTCCTGTTTTTTTGGTCCGGCTCAT	1161
Db	1	GTAAACACCCCGCCCTCCTCTCTTCTCTCGTTTTTTTGGTCTCGAT	60
Qy	1162	CTTTGACCTTGTAATGTGGGTGGACAGACGGCTTCTGTGCCAATCGTTCGGCGG	1221
Db	61	CTTTGGCCTTGTAATGTGGGTGGACAGCGCTTCTGTGCCAATCGTTCGGCGG	120
Qy	1222	AGGGCGGGATCTTCGCGGCTTGGCGTCTCCGCGGTGATCGGCCCGATCTCGCGGGA	1281
Db	121	AGGGCGGGATCTTCGCGGCTTGGCGTCTCCGCGGTGATCGGCCCGATCTCGCGGGA	180
Qy	1282	ATGGGGGCTCCGAGTGTAGATCTGATCCGCGCTTGTGGGGGAGATATGGGGGCTTTAA	1341
Db	181	ATGGGGGCTCTCGAGTGTAGATCTGATCCGCGCTTGTGGGGGAGATATGGGGGCTTTAA	240
Qy	1342	AATTTCCGCATGCTAAACAAGATCAGGAGAGGGGAAAAGGCACTATGTTTTATATTTT	1401
Db	241	AATTTCCGCATGCTAAACAAGATCAGGAGAGGGGAAAAGGCACTATGTTTTATATTTT	300
Qy	1402	TATATATTTCTGCTGCTGCTGCTCAGGCTTAGATGTCTAGATCTTTCTTTCTTTT	1461

Db 301 TATATATTTCCTGCTGCTGCTGAGGCTTAAGTATGCTAGAACCTTTCTTTCTCTTTT 360

Qy 1462 GTGGGTAAATTTTGAATCCCTCAGACATTTTATCCGTAGTTTTTTTCAATGATTGT 152

Db 361 GTGGGTAAATTTGAATCCCTCAGACATTTTATCCGTAGTTTTTTCTTTCAATGATTGT 420

Qy 1522 GACAAATGACGCTCTGTGCGGAGCTTTTTTTGTG 1555

Db 421 GACCAATGACGCTCTGTGCGGAGCTTTTTTTGTG 454

RESULT 4
US-08-144-602B-6

PatentNo. 5641876
GENERAL INFORMATION:
APPLICANT: MCELROY, David
APPLICANT: Wu, Ray
TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: CLINTON SQUARE, P.O. BOX 1051
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/144,602B
FILING DATE: 27-OCT-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/10140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-144-602B-6

Query Match	27.4%	Score	428.8;	DB 1,	Length	1392;
Best Local Similarity	84.9%;	Pred. No.	2.3e-108;			
Matches 518; Conservative	0;	Mismatches	82;	Indels	10;	Gaps
						3;

OY	958	CATGCACCTACTGCGCCAAATTCGCCGAATAATCAACAGCCTCCCAATTCCACGGTGCACACA	1017
Dd	775	CAAGAANAAGCCCCCATGTGCACATATATACATACCCCCCCTCTCTCCATCCCCCCA	834
OY	1018	ACTGCGCGTCTCTCGCGCGCCAAAGCACAAAGGATTTGGCCGACACCGCGGTGAGTCTCTC	1077
Dd	835	AACCTAACACACACACACACACACTCTCTCCCCCTCTGCTGCGCGAAGACGAGTCTCTC	894
OY	1078	CCCCCTCCCCCTCGCGCGCGCGCGGTAAACAACCCGC--CCCTCCCTCTTTCTTCCC	1135
Dd	895	CCCCCTCCCCCTCGCGCGCGCGCGGTAAACACACCCGCGTCTCTCTCTTTCTTCTCC	954
OY	1136	GTTTTTTTTTTCGTCGTCCGCTCTGCATCTTTGGCTTTGGTAGTTTGAGTGAGCGAGACGGG	1195
Dd	955	GTTTTTTTTTTCGTCGTCCGCTCTGCATCTTTGGCTTTGGTAGTTTGAGGAGCGAGAG-GGGG	1013
OY	1196	CTTCGTGCGCCAGATCGGTGCGCGGAGAGGCGCGAGATCTCGCGAGCTCTCCGAGCG	1255

Db	1014	CTTCGTGCGCCAGATCGGTGCGCGAGGGGGAGATCTGGCGGCTGG-----GTCTC	1066
Qy	1256	TGAGTCGGCCCGGATCTCGGGGGGAATGGGGCTCTGGATGTAGATCTGATCGGCCGTT	1315
Db	1067	GGCGTGGGGCGCGGATCTCGCGGGGAATGGGGCTCTGGATGTAGATCTGATCGGCCGTT	1126
Qy	1316	GTTGGGGGAGATGATGGGGCGTTTAAATTTGGCATGCTAAACAATCAGAAAGAGGG	1375
Db	1127	GTTGGGGGAGATGATGGGGCGTTTAAATTTGGCATGCTAAACAATCAGAAAGAGGG	1186
Qy	1376	GAAGAAGGCACTATGTTTATTTATTTATTTATTTCTGCTGCTGCTGCTGACGCTTAGAT	1435
Db	1187	GAAGAAGGCACTATGTTTATTTATTTATTTATTTCTGCTGCTGCTGCTGACGCTTAGAT	1246
Qy	1436	GTGCTAATCTTCTTCTTCTTTTGTGGGTGAATTGAATCCGACGATTGTTCAT	1495
Db	1247	GTGCTAATCTTCTTCTTCTTTTGTGGGTGAATTGAATCCGACGATTGTTCAT	1306
Qy	1496	CGGTAGTTTTTCTTTTCATGATTTGTGACAACAATGCACCTCGTGGAGCTTTTGTAG	1555
Db	1307	CGGTAGTTTTTCTTTTCATGATTTGTGACAACAATGCACCTCGTGGAGCTTTTGTAG	1366
Qy	1556	GTAGACCATG	1565
Db	1367	GTAGACCATG	1376

RESULT 5
US-08-14-602B-7
; Sequence 7, Application US/08144602B

1 APPLICANT: McElroy, David
 2 APPLICANT: Wu, Ray
 3 TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
 4 NUMBER OF SEQUENCES: 27
 5 CORRESPONDENCE ADDRESS:
 6 ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
 7 STREET: CLINTON SQUARE, P.O. BOX 1051
 8 CITY: ROCHESTER
 9 STATE: NEW YORK
 10 COUNTRY: USA
 11 ZIP: 14603
 12
 13 COMPUTER READABLE FORM:
 14 MEDIUM TYPE: Floppy disk
 15 COMPUTER: IBM PC compatible
 16 OPERATING SYSTEM: PC-DOS/MS-DOS
 17 SOFTWARE: PatentIn Release #1.0, Version #1.30
 18
 19 CURRENT APPLICATION DATA:
 20 APPLICATION NUMBER: US/08/144,602B
 21 FILING DATE: 27-OCT-1993
 22 CLASSIFICATION: 536
 23 ATTORNEY/AGENT INFORMATION:
 24 NAME: TIMIAN, SUSAN J.
 25 REGISTRATION NUMBER: 34,103
 26 REFERENCE/DOCKET NUMBER: 19603/10140
 27 TELECOMMUNICATION INFORMATION:
 28 TELEPHONE: 716-263-1636
 29 TELEFAX: 716-263-1600
 30
 31 INFORMATION FOR SEQ ID NO: 7:
 32 SEQUENCE CHARACTERISTICS:
 33 LENGTH: 1404 base pairs
 34 TYPE: nucleic acid
 35 STRANDEDNESS: single
 36 TOPOLOGY: linear
 37
 38 MOLECULE TYPE: cDNA
 39
 40 US-08-144-602B-7

Query Match	27.4%	Score 428.8	DB 1	Length 1404
Best Local Similarity	84.9%	Pred. NO. 2.3e-108		
Matches 518; Conservative	0	Mismatches 82	Indels 10	Gaps 3

QY 958 CATGCATCACTGCGAAATCCCGAAGAAATCAACATCCCATTCAGCGTCCACCA 1017
DB 785 CAAAGAAACGCCCCCATCGCATATATACATACCCCCCTCTCTCCATCCCCCA 844
QY 1018 ACTGCGGTCCTCGCGCCCAAGCAACAAAGAAATGGCCCGCAGCGGTGAGCTCTC 1077
DB 845 ACCCTACACACACACACACACACCTCTCCCGCCCTGCTCGCGAGACGAGCTCTC 904
QY 1078 CCCCCCTCCCTCGCGCGCGCGGTAAACACCCCGC-CCCTCTCTCTCTCTCTCTC 1135
DB 905 CCCCCCTCCCTCGCGCGCGCGGTAAACACCCCGCGTCTCTCTCTCTCTCTCTC 964
QY 1136 GTTTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1195
DB 965 GTTTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1023
QY 1196 CTTGCTGCGCCAGATCGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1255
DB 1024 CTTGCTGCGCCAGATCGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1076
QY 1256 TGAATCGGCGCGGATCTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1315
DB 1077 GCGCTGCGCGCGGATCTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1136
QY 1316 GTTGGGAGAGATGATGGGCGGTTTAAATTTGCGCATGCTAAACAAGATCAGGAAGGG 1375
DB 1137 GTTGGGAGAGATGATGGGCGGTTTAAATTTGCGCATGCTAAACAAGATCAGGAAGGG 1196
QY 1376 GAAAGGAGCATAGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1435
DB 1197 GAAAGGAGCATAGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1256
QY 1436 GTGCTAGATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1495
DB 1257 GTGCTAGATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1316
QY 1496 CGTAGTATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1555
DB 1317 CGTAGTATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1376
QY 1556 GTAGACCATG 1565
DB 1377 GTAGACCATG 1386

RESULT 6
US-08-144-602B-5
Sequence 5, Application US/08144602B
Patent No. 5641876
GENERAL INFORMATION:
APPLICANT: McElroy, David
APPLICANT: Wu, Ray
TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: CLINTON SQUARE, P.O. BOX 1051
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/144,602B
FILING DATE: 27-OCT-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/10140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2199 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-144-602B-5

Query Match 27.4%; Score 428.8; DB 1; Length 2199;
Best Local Similarity 84.9%; Pred. No. 3e-108;
Matches 518; Conservative 0; Mismatches 82; Indels 10; Gaps 3;

QY 958 CATGCATCACTGCGAAATCCCGAAGAAATCAACATCCCATTCAGCGTCCACCA 1017
DB 1582 CAAAGAAACGCCCCCATCGCATATATACATACCCCCCTCTCTCCATCCCCCA 1641
QY 1018 ACTGCGGTCCTCGCGCCCAAGCAACAAAGAAATGGCCCGCAGCGGTGAGCTCTC 1077
DB 1642 ACCCTACACACACACACACACACCTCTCCCGCCCTGCTCGCGAGACGAGCTCTC 1701
QY 1078 CCCCCCTCCCTCGCGCGCGCGGTAAACACCCCGC-CCCTCTCTCTCTCTCTCTC 1135
DB 1702 CCCCCCTCCCTCGCGCGCGCGGTAAACACCCCGCGTCTCTCTCTCTCTCTCTC 1761
QY 1136 GTTTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1195
DB 1762 GTTTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1820
QY 1196 CTTGCTGCGCCAGATCGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1255
DB 1821 CTTGCTGCGCCAGATCGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1873
QY 1256 TGAATCGGCGCGGATCTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1315
DB 1874 GCGCTGCGCGCGGATCTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1933
QY 1316 GTTGGGAGAGATGATGGGCGGTTTAAATTTGCGCATGCTAAACAAGATCAGGAAGGG 1375
DB 1934 GTTGGGAGAGATGATGGGCGGTTTAAATTTGCGCATGCTAAACAAGATCAGGAAGGG 1993
QY 1376 GAAAGGAGCATAGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1435
DB 1994 GAAAGGAGCATAGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 2053
QY 1436 GTGCTAGATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1495
DB 2054 GTGCTAGATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 2113
QY 1496 CGTAGTATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1555
DB 2114 CGTAGTATTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 2173
QY 1556 GTAGACCATG 1565
DB 2174 GTAGACCATG 2183

RESULT 7
US-08-144-602B-4
Sequence 4, Application US/08144602B
Patent No. 5641876
GENERAL INFORMATION:
APPLICANT: McElroy, David
APPLICANT: Wu, Ray
TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP

STREET: CLINTON SQUARE, P.O. BOX 1051
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/144,602B
FILING DATE: 27-OCT-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/10140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-144-602B-4

Query Match 27.4%; Score 428.8; DB 1; Length 5643;
Best Local Similarity 84.9%; Pred. No. 5,2e-108;

Matches 518; Conservative 0; Mismatches 82; Indels 10; Gaps 3;

QY 958 GATGCGATCACTGCGCAATCCCGGAGAAATCAACACTTCCCAATTCACGCTGCCACCA 1017
Db 1585 CAAAGAAACGCCCCCGCATCGCCACTATATATACATACCCCCCTCTCTCCATCCCCCA 1644
QY 1018 ACTGCGGCTCTCGCGCCAGACCAAGAAATGGCGCCACCGCGGTGGAGCTTC 1077
Db 1645 ACCCTACACACACACACACACACCTCTCCCCCTGCTGCGAGCGAGCTCTTC 1704
QY 1078 CCCCCTCCCTCGCGCGCGCGGTAACCAACCCCGC--CCCTCTCTCTCTCTCTCC 1135
Db 1705 CCCCCTCCCTCGCGCGCGCGGTAACCAACCCCGGCTCTCTCTCTCTCTCTCC 1764
QY 1136 GTTTTTTTTTCTGCTCGTCTCGATCTTTTGCCCTTGTGATTTGGTGGGCAAGCGG 1195
Db 1765 GTTTTTTTTTCTGCTCGTCTCGATCTTTTGCCCTTGTGATTTGGGCGAGAG- GCGG 1823
QY 1196 CTTCGTCGCCAATCGGTGCGGCGGAGCGGAGATCTCGCGCTGCGCTCCCGGCG 1255
Db 1824 CTTCGTCGCCAATCGGTGCGGCGGAGCGGAGATCTCGCGCTGCGCTGCGG-----GTC 1876
QY 1256 TGAATGCGCCGGAATCTCGCGGGAATGGGCTCTCGATGTAGATCTGATCCGCGCT 1315
Db 1877 GGGGTGCGCGGATCTCTCGCGGGAATGGGCTCTCGATGTAGATCTGATCCGCGCT 1936
QY 1316 GTTGGGGAGATGATGGGGCGTTTAAATTTCCGATGCTAAACAAGATCAGGAAGAGG 1375
Db 1937 GTTGGGGAGATGATGGGGCGTTTAAATTTCCGATGCTAAACAAGATCAGGAAGAGG 1996
QY 1376 GAAAAGGCACTATGTTTAT 1435
Db 1997 GAAAAGGCACTATGTTTAT 2056
QY 1436 GTGCTAGATCTTTCT 1495
Db 2057 GTGCTAGATCTTTCT 2116
QY 1496 CGGTAGTTTTCTTTTCATGATTTGTGACAAATGACAGCTCTGTCGGAGCTTTTGTAG 1555
Db 2117 CGGTAGTTTTCTTTTCATGATTTGTGACAAATGACAGCTCTGTCGGAGCTTTTGTAG 2176

QY 1556 GTAGACCATG 1565
Db 2177 GTAGAGATG 2186

RESULT 8
US-09-078-862-5
Sequence 5, Application US/0907862
Patent No. 6091003
GENERAL INFORMATION:
APPLICANT: Nan, Guo-Ling
APPLICANT: Nagai, Chifumi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC
TITLE OF INVENTION: TRANSFORMATION OF PINEAPPLE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,862
FILING DATE: 14-MAY-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: US-03321
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 623 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-078-862-5

Query Match 27.2%; Score 426.2; DB 3; Length 623;
Best Local Similarity 87.3%; Pred. No. 7,4e-108;

Matches 504; Conservative 0; Mismatches 63; Indels 10; Gaps 3;

QY 991 ACACTCCCAATTCACGCTGCGCACCACTGCGCTCTCGCGCGCAAGACCAAGAA 1050
Db 10 ACCCCCCCT 69
QY 1051 TTGGCGCACCGCGGTGAGTCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 1110
Db 70 CCTCGCTCGCGAGACGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 129
QY 1111 CCGC--CCCT 1168
Db 130 CCGCT 189
QY 1169 CTGTGATTTGGTGGGCGAGAGCGGCTCTGCGCCAGATCGGTGCGGAGGAGGCG 1228
Db 190 CTGTGATTTGGGCGGAGAG- GCGGCTTCTGCGCCAGATCGGTGCGGAGGAGGCG 248
QY 1229 GGATCTCGCGGCTGCGCTCTCCGCGGTGAGTCTGCGCCGAGATCTCTGCGGGAATCGGCG 1288
Db 249 GGATCTCGCGGCTGCG-----GTCGCGCGTGGCGCGGATCTCTGCGGGAATGGGCG 301


```
Qy 1289 TCTCGAGTATGATCTGATCCGCTGTTGGGGGAGATGAGGGGCGTTTAAATTTCG 1348
    |||
Db 302 TCTCGAGTATGATCTATCCGCGCTGTGGGGGAGATGAGGGGCGTTTAAATTTCG 361
Qy 1349 CCATGCTAAACAAGATCAGGAAGAGGAGAAAGGCACTATGCTTTATATTTATATAT 1408
    |||
Db 362 CCATGCTAAACAAGATCAGGAAGAGGAGAAAGGCACTATGCTTTATATTTTATATAT 421
Qy 1409 TTCTGCTGCTGCTGCTGAGGCTTATGATGCTAGATCTTTCTTTCTTTTGTGGGTA 1468
    |||
Db 422 TTCTGCTGCTGCTGCTGAGGCTTATGATGCTAGATCTTTCTTTCTTTTGTGGGTA 481
Qy 1469 GAATTTGAATCCCTCAGCAATTTGTCATCGGTAATTTTCTTTCATGATTTTGAACAAT 1528
    |||
Db 482 GAATTTGAATCCCTCAGCAATTTGTCATCGGTAATTTTCTTTCATGATTTTGAACAAT 541
Qy 1529 GCAGCCTGTCGAGGCTTTTGTAGTGAACCATG 1565
    |||
Db 542 GCAGCCTGTCGAGGCTTTTGTAGTGAACCATG 578
```

RESULT 9

```
US-09-068-101-5
; Sequence 5, Application US/09068101
; Patent No. 6372960
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2121-139P
; CURRENT APPLICATION NUMBER: US/09/068, 101
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: EP 96202446.9
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pmv71"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1999)..(3400)
; OTHER INFORMATION: label = PRA1, "promoter region of rice actin gene
; OTHER INFORMATION: - contains an intron in the leader"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3401)..(3676)
; OTHER INFORMATION: label = barstar, "barstar DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3677)..(4003)
; OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
; OTHER INFORMATION: T-DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3399)..(3404)
; OTHER INFORMATION: label = NcoI, "NcoI recognition site"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4015)..(4021)
; OTHER INFORMATION: label = KpnI, "KpnI recognition site"
US-09-068-101-5
```

```
Query Match 24.2%; Score 378.4; DB 3; Length 4032;
Best Local Similarity 87.1%; Pred. No. 4e-94;
Matches 498; Conservative 0; Mismatches 61; Indels 13; Gaps 7;
Qy 1004 CCAGCGCCACCAACTCGCGTCTCCGCGCCACCAAGCAATTTGGCCGCCACCG 1063
    |||
```

```
Db 2835 CAACCTACACCAACCACCAACCACTCACTCCCTCCCTGCTGCGGACGAG 2894
Qy 1064 CGGTGAGCTCTCTCCCTCTCCCTCCCTGCGCGCGCGGTAAACACCCGCCCTCTCT 1123
Db 2895 AGCTCTCTCCCTCTCCCTCTCCCTCCCTGCGCGCGCGGTAAACACCCGCCCTCTCT 2953
Qy 1124 CTTTCTTTCGCGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1182
    |||
Db 2954 CTTTCTTTCGCGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1246
Qy 1183 TGGGCGAGA----GCGGCTTCTGCGCCAGATCGTGCAGGAGGCGGAGTCTCGCG 1238
    |||
Db 3014 TGGGCGAGAAGGCGGCTTCTGCGCGCGCCAGATCGTGCAGGAGGCGGAGTCTCGCG 3073
Qy 1239 GCTGCGCTCTCG--GCGGTGATCGGCGCGGATCTCTCGGCGGAATGGGCGTCTCGAT 1296
    |||
Db 3074 GCTGCGGCTCTCGCGCGCGGCTGATCGGCGCGGATCTCTCGGCGGAATGGGCGTCTCGAT 3133
Qy 1297 GTPGATCT--GATCCCGCTTGTGTGGGAGATGATGAGGCGCTTAAATTT--CGGCATG 1353
    |||
Db 3134 GTAGATCTCGATCTCGCGCTTGTGTGGGAGATGATGAGGCGCTTAAATTTTCCGCATG 3193
Qy 1354 CTAAACAAGATCAGGAAGAGGAGAAAGGCACTATGCTTTATATTTATATTTCTG 1413
    |||
Db 3194 CTAAACAAGATCAGGAAGAGGAGAAAGGCACTATGCTTTATATTTATATTTCTG 3253
Qy 1414 CTGCTGCTGCTCAGGCTTATGATGCTAGATCTTTCTTTCTTTTGTGGGTAGATTT 1473
    |||
Db 3254 CTGCT--TGTGAGGCTTATGATGCTAGATCTTTCTTTCTTTTGTGGGTAGATTT 3311
Qy 1474 TGAATCCCTCAGATGTTTATGATGCTTTTCTTTCTTTTCTTTCTTTTCTTTTCTTT 1533
    |||
Db 3312 TGAATCCCTCAGATGTTTATGATGCTTTTCTTTCTTTTCTTTCTTTTCTTTTCTTT 3371
Qy 1534 CTGCTGCGAGGCTTTTGTAGTGAACCATG 1565
    |||
Db 3372 CTGCTGCGAGGCTTTTGTAGTGAACCATG 3403
```

RESULT 10

```
US-09-970-921-5
; Sequence 5, Application US/09970921
; Patent No. 6789575
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pmv71"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1999)..(3400)
; OTHER INFORMATION: label = PRA1, "promoter region of rice actin gene
; OTHER INFORMATION: - contains an intron in the leader"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3401)..(3676)
; OTHER INFORMATION: label = barstar, "barstar DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3677)..(4003)
; OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
; OTHER INFORMATION: T-DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3399)..(3404)
; OTHER INFORMATION: label = NcoI, "NcoI recognition site"
```

```
; NAME/KEY: misc feature
; LOCATION: (4016)..(4021)
; OTHER INFORMATION: label = kpn1, "kpn1 recognition site"
US-09-970-921-5
```

```
Query Match          24.2%; Score 378.4; DB 4; Length 4032;
Best Local Similarity 87.1%; Pred. No. 4e-94;
Matches 498; Conservative 0; Mismatches 61; Indels 13; Gaps 7;
```

```
QY 1004 CCAAGCTGACCAACTCCGCGCTCCCGGCAAGACCAAGAAATGGCCGCCACCG 1063
DB 2835 CAACCCCTACACACACACACACACACACCTCCCTCCCTCCGCTGCGAGAGAG 2894
QY 1064 CCGTGGAGCTCTCCCGCCCTCCCGCCGCGCGCGGAGAACACCCCGCCCTCTCT 1123
DB 2895 AGCTCTCCCGCCCTCCCGCCCTCCCGCCGCGCGCGGAGAACACCCCGCCCTCTCT 2953
QY 1124 CTCTCTCTCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1182
DB 2954 CTCTCTCTCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3013
QY 1183 TGGGCGGAGA---GCGGCTCTGCTGCGCCCAATCGGTGCGGAGGCGGAGATCTCGCG 1238
DB 3014 TGGGCGGAGGCGGCTCTGCGCGCGCCCAATCGGTGCGGAGGCGGAGATCTCGCG 3073
QY 1239 GCTGGCGCTCTCGG--GCGTGAATCGGCGCGGATCTCGGCGGAAATGGGGCTCTCGGAT 1296
DB 3074 GCTGGGCGCTCTCGCGCGCGCGGATCTCGGCGGAAATGGGGCTCTCGGAT 3133
QY 1297 GTAGATCT--GATCCGCGCTGTTGGGAGATGATGAGGCGCTTAAATTT--CGCCATG 1353
DB 3134 GTAGATCTGCGATCCGCGCTGTTGGGAGATGATGAGGCGCTTAAATTT--CGCCATG 3193
QY 1354 CTAAACAATGAGGAAGAGGGAAGAGGCACTATGCTTATTTTATTTATTTCTG 1413
DB 3194 CTAAACAATGAGGAAGAGGGAAGAGGCACTATGCTTATTTTATTTATTTCTG 3253
QY 1414 CTGCTGCTGCTGAGGCTTAGATGCTAGATCTTTCTTTCTTTTGGGGTAGAAT 1473
DB 3254 CTGCT--TGTGAGGCTTAGATGCTAGATCTTTCTTTCTTTTGGGGTAGAAT 3311
QY 1474 TGAATCCCTCAGCATTTGTCATCGTAGTTTCTTTCTTATGATTTGTGAACAATGACG 1533
DB 3312 TGAATCCCTCAGCATTTGTCATCGTAGTTTCTTTCTTATGATTTGTGAACAATGACG 3371
QY 1534 CTGCTGCGAGGCTTTTGTAGGTAGACCATG 1565
DB 3372 CTGCTGCGAGGCTTTTGTAGGTAGACCATG 3403
```

```
RESULT 11
US-09-377-466B-19
; Sequence 19, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: Promoter
; LOCATION: (14)..(235)
; OTHER INFORMATION: P-CamV.AS4
; NAME/KEY: 5'UTR
```

```
; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: Intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Os.Act1
; NAME/KEY: CDS
; LOCATION: (811)..(2769)
; OTHER INFORMATION: Cry3Bb1 variant 11231mw1
; NAME/KEY: terminator
; LOCATION: (2787)..(3020)
; OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-19
```

```
Query Match          24.0%; Score 375.8; DB 4; Length 3039;
Best Local Similarity 93.2%; Pred. No. 1.8e-93;
Matches 450; Conservative 0; Mismatches 22; Indels 11; Gaps 5;
```

```
QY 1087 CCTCCGCGCGCGCGGTAACACACCCCGCCCTCTCTCTCTCTCTCTCTCTCTCT 1146
DB 319 CCTCCGCGCGCGCGGTAACACACCCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCT 378
QY 1147 CGTCTCGCTCGATCTTTGGCTTGTAGATTGGGTGGGCGAGA---GCGGCTTCGT 1202
DB 379 CGTCTCGCTCGATCTTTGGCTTGTAGATTGGGTGGGCGAGA---GCGGCTTCGT 438
QY 1203 GCCAGATCGTGGCGGAGGAGGCGGATCTCGGCGCTGCGCTCCG--GCGGTGAGT 1260
DB 439 GCCAGATCGTGGCGGAGGAGGCGGATCTCGGCGCTGCGGCTTCGCGCGCGGTGAT 498
QY 1261 CGGCGCGATCTCGGCGGGAATGGGCGCTCTCGATGATGATCT--GATCCGCGCTTGT 1318
DB 499 CGGCGCGATCTCGGCGGGAATGGGCGCTCTCGATGATGATCTCGATCTCCGCTTGT 558
QY 1319 GGGGAGATGATGGGCGCTTAAATTT--CGCATGCTAAACAATGAGAGGGGA 1377
DB 559 GGGGAGATGATGGGCGCTTAAATTTCCGCGCTAAACAATGAGAGGGGA 618
QY 1378 AAAGGCACTATGATTTATTTATTTATTTATTTCTGCTGCTGCTGCTGCTGCTGCT 1437
DB 619 AAAGGCACTATGATTTATTTATTTATTTATTTCTGCTGCT--TGTGAGGCTTGTAGAT 676
QY 1438 GCTAGATCTTTCTTTCTTTTGTGGTAGAATTTGAATCTTCAGATTTTCATCG 1497
DB 677 GCTAGATCTTTCTTTCTTTTGTGGTAGAATTTGAATCTTCAGATTTTCATCG 736
QY 1498 GTAGTTTTCTTTTATGATTTGTGAACAATGCACTCGTGGAGGCTTTTGTAGGT 1557
DB 737 GTAGTTTTCTTTTATGATTTGTGAACAATGCACTCGTGGAGGCTTTTGTAGGT 796
QY 1558 AGA 1560
DB 797 AGA 799
```

```
RESULT 12
US-09-377-466B-21
; Sequence 21, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette
```

```

;
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 38
;
; LENGTH: 3044

```

```

:
:
: FILE REFERENCE: 38-21 (15304) Ctr3Bb Improved Exp. Corn
:
: CURRENT APPLICATION NUMBER: US/09/377,466B
:
: CURRENT FILING DATE: 1999-08-19
:
: NUMBER OF SEQ. ID. NOS. 42
:

```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 02:27:12 ; Search time 1992.88 Seconds
(without alignments)
5157.238 Million cell updates/sec

Title: US-10-758-799-3
Perfect score: 1565
Sequence: 1 GAATTCCTCGAGCTGACCG.....TTTTTGTAGTACACATG 1565

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
17: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
18: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
19: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
20: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
21: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
22: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
23: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*
24: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1565	100.0	9	US-09-037-531-3	Sequence 3, Appli
2	1565	100.0	19	US-10-758-799-3	Sequence 1, Appli
3	1021	65.2	9	US-09-037-531-1	Sequence 1, Appli
4	1021	65.2	19	US-10-758-799-1	Sequence 1, Appli
5	454	29.0	9	US-09-037-531-2	Sequence 2, Appli
6	454	29.0	19	US-10-758-799-2	Sequence 2, Appli
7	426.2	27.2	9	US-09-981-900B-19	Sequence 19, Appli

	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45																																																																																																																																																																																																										
c	402.8	25.7	2480	21	US-10-678-588A-1	Sequence 1, Appli	402.8	25.7	5365	22	US-10-839-092-57	Sequence 57, Appli	392.8	25.1	1384	22	US-10-839-092-35	Sequence 35, Appli	392.8	25.0	7943	10	US-09-845-064-15	Sequence 15, Appli	392.8	25.0	7943	10	US-09-845-064-12	Sequence 12, Appli	392.8	25.0	10003	10	US-09-845-064-21	Sequence 21, Appli	390.4	24.9	470	16	US-10-087-167-109	Sequence 109, App	384.8	24.6	9359	21	US-10-344-977A-1	Sequence 1, Appli	384.8	24.6	9359	22	US-10-344-975B-1	Sequence 1, Appli	381.2	24.4	7794	24	US-11-057-062-2	Sequence 2, Appli	381.2	24.4	8590	24	US-11-057-062-1	Sequence 1, Appli	378.8	24.2	4032	9	US-09-970-921-5	Sequence 5, Appli	378.8	24.1	1597	22	US-10-839-092-50	Sequence 50, Appli	375.8	24.0	491	9	US-09-376-940-50	Sequence 34, Appli	375.8	24.0	3039	20	US-10-841-796-34	Sequence 34, Appli	375.8	24.0	3039	15	US-10-232-665-19	Sequence 19, Appli	375.8	24.0	3039	15	US-10-232-665-21	Sequence 21, Appli	375.8	24.0	3044	15	US-10-232-665-38	Sequence 38, Appli	375.8	24.0	3044	15	US-10-232-665-36	Sequence 36, Appli	375.8	24.0	3455	15	US-10-232-665-17	Sequence 17, Appli	375.8	24.0	3455	15	US-10-232-665-23	Sequence 23, Appli	375.8	24.0	3469	15	US-09-845-064-13	Sequence 13, Appli	375.8	24.0	6865	10	US-09-845-064-21	Sequence 21, Appli	375.8	24.0	10003	10	US-09-841-796-33	Sequence 33, Appli	375.8	22.9	11546	20	US-10-841-796-33	Sequence 27, Appli	358.8	22.9	8296	24	US-11-057-062-1	Sequence 1, Appli	358.8	22.9	8296	24	US-11-057-062-1	Sequence 1, Appli	352.8	22.5	4176	15	US-10-213-791-29	Sequence 29, Appli	352.8	22.5	4176	15	US-10-213-791-25	Sequence 25, Appli	310.2	19.8	2122	15	US-10-213-791-25	Sequence 25, Appli	310.2	19.8	2122	15	US-09-991-209-43	Sequence 43, Appli	247.8	15.8	4773	10	US-09-991-209-32	Sequence 32, Appli	247.8	15.8	4773	10	US-09-991-209-34	Sequence 34, Appli	247.8	15.8	4950	10	US-09-991-209-37	Sequence 37, Appli	247.8	15.8	4965	10	US-09-991-209-35	Sequence 35, Appli	247.8	15.8	4974	10	US-09-991-209-36	Sequence 36, Appli	247.8	15.8	5164	10	US-09-991-209-25	Sequence 25, Appli	247.8	15.8	5277	10	US-09-991-209-25	Sequence 25, Appli	247.8	15.8	5285	10	US-09-991-209-38	Sequence 38, Appli	247.8	15.8	5327	10	US-09-991-209-27	Sequence 27, Appli

ALIGNMENTS

RESULT 1
US-09-037-531-3
; Sequence 3, Application US/09037531
; Patent No. US20020104117A1
; GENERAL INFORMATION:
; APPLICANT: DeRose, Richard
; TITLE OF INVENTION: Fireyasin, Georges
; TITLE OF INVENTION: Maltz H3C4 Promoter Combined With The
; TITLE OF INVENTION: Firet Inction Of Rice Actin, Chimeric Gene Comprising It
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037, 531
; FILING DATE: 10-MAR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G.
; REGISTRATION NUMBER: 30962

```
REFERENCE/DOCKET NUMBER: 5500*24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)658-9141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-037-531-3

Query Match      100.0%; Score 1565; DB 9; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTCCTGACAGTGCAGGATCCCTTATGTGCAACATTACTGTATGATATCAT 60
DB 1 GAATTCCTGACAGTGCAGGATCCCTTATGTGCAACATTACTGTATGATATCAT 60
QY 61 TTAATTGAATAGAACTTTCTATATCTCTTACTAACAATAATCTGTGTTTAAAT 120
DB 61 TTAATTGAATAGAACTTTCTATATCTCTTACTAACAATAATCTGTGTTTAAAT 120
QY 121 TCAGTCTCAACATTCATGCTCAAGTATAGTGAAGTCAAAATTTACTATTAT 180
DB 121 TCAGTCTCAACATTCATGCTCAAGTATAGTGAAGTCAAAATTTACTATTAT 180
QY 181 TTCTCATATTTTTTCTTATATACATTTTGGCCCTTACAAATCATCATATATCA 240
DB 181 TTCTCATATTTTTTCTTATATACATTTTGGCCCTTACAAATCATCATATATCA 240
QY 241 TCCCTTCCGCTGCTCTTAAAGATTCATCCCTGAATCTTATCTCTCCAAATACGT 300
DB 241 TCCCTTCCGCTGCTCTTAAAGATTCATCCCTGAATCTTATCTCTCCAAATACGT 300
QY 301 TCTCTAATACAGTCTCTATATACAAATCCTATATTAGAGACATTTTATTTTGTAC 360
DB 301 TCTCTAATACAGTCTCTATATACAAATCCTATATTAGAGACATTTTATTTTGTAC 360
QY 361 ATACATATTTTGCATCTCTCAATGCAATTAATATTTTATCTTAAACCGATAT 420
DB 361 ATACATATTTTGCATCTCTCAATGCAATTAATATTTTATCTTAAACCGATAT 420
QY 421 TTAAGATTCAGAAAGGATGAAAGCTGTTAGATAATCTATATATAGAAATCCAGT 480
DB 421 TTAAGATTCAGAAAGGATGAAAGCTGTTAGATAATCTATATATAGAAATCCAGT 480
QY 481 AGCGTTCTCTAATTTAGATGATTTATTAGAGACGCTGTAGAAAAAGTAAATTC 540
DB 481 AGCGTTCTCTAATTTAGATGATTTATTAGAGACGCTGTAGAAAAAGTAAATTC 540
QY 541 TTGATTATTTATATTTAGGATAGTAGCCCTTATATGCTTTATATAGATCTTTGTGACCA 600
DB 541 TTGATTATTTATATTTAGGATAGTAGCCCTTATATGCTTTATATAGATCTTTGTGACCA 600
QY 601 GCGTTATACCGGTTATTTTGGCATTGGCGCTCTCATTTTCACTCCAGGCCCAATTT 660
DB 601 GCGTTATACCGGTTATTTTGGCATTGGCGCTCTCATTTTCACTCCAGGCCCAATTT 660
QY 661 TCACGTTTTCACGGAAGCGCCAGCTGCTTAACCAACAATTTGTACGCTGCGGTT 720
DB 661 TCACGTTTTCACGGAAGCGCCAGCTGCTTAACCAACAATTTGTACGCTGCGGTT 720
QY 721 TTCAAAAGAGTGCAGAAACCATCTGCAACCGAGTAGAGCCCTCGGATCTCCCTG 780
DB 721 TTCAAAAGAGTGCAGAAACCATCTGCAACCGAGTAGAGCCCTCGGATCTCCCTG 780
QY 781 ATTAAGTCTTACGCAATAGAGCCCAAGAACCATCTACAGCGGATGTCTTACGCTTC 840
DB 781 ATTAAGTCTTACGCAATAGAGCCCAAGAACCATCTACAGCGGATGTCTTACGCTTC 840
QY 841 CACCTCATCGGCGCGCTCATCTCCATCAACACCTATCTCGTTACCTTCCATCTCC 900
```

```
|||||
DB 841 CACCTCATCGGCGCGCTCATCTCCATCAACACCTATCTCGTTACCTTCCATCTCC 900
QY 901 GAAAAAATTTCTGGGTCCGCTCCGACCTACTAATAATACCATCCATACAGCGAT 960
DB 901 GAAAAAATTTCTGGGTCCGCTCCGACCTACTAATAATACCATCCATACAGCGAT 960
QY 961 CGCATCACTGCAAAATCCCAAGAAATCAACACCTCCAAATTCACAGCTGCACAACT 1020
DB 961 CGCATCACTGCAAAATCCCAAGAAATCAACACCTCCAAATTCACAGCTGCACAACT 1020
QY 1021 CGCGTCTCTCGGCGCAAGACCAAGAAATTTGCGCCACCGCGGTGAGTCTCTCCC 1080
DB 1021 CGCGTCTCTCGGCGCAAGACCAAGAAATTTGCGCCACCGCGGTGAGTCTCTCCC 1080
QY 1081 CCTCCCTCTCGGCGCGCGCGGTATCAACCCCGCCCTCTCTCTTTCTTCTCGGTTT 1140
DB 1081 CCTCCCTCTCGGCGCGCGCGGTATCAACCCCGCCCTCTCTCTTTCTTCTCGGTTT 1140
QY 1141 TTTTTCGTCGTGATCTGATCTTGGCTTGGTGGTGGGCGAGAGCGGCTTCG 1200
DB 1141 TTTTTCGTCGTGATCTGATCTTGGCTTGGTGGTGGGCGAGCGGCTTCG 1200
QY 1201 TCGCCCAATCGGTGCGGCGAGCGGATCTCGCGGCTGCGCTTCGCGGCTGAGT 1260
DB 1201 TCGCCCAATCGGTGCGGCGAGCGGATCTCGCGGCTGCGCTTCGCGGCGTGA 1260
QY 1261 CGGCGCGGATCTCGCGGCGGAAATGGGGGCTCTCGAATGATATGATCCGCGTGG 1320
DB 1261 CGGCGCGGATCTCGCGGCGGAAATGGGGGCTCTCGAATGATATGATCCGCGTGG 1320
QY 1321 GGGAGATGATGGGGGCTTTAAATTTCCCATGCTAAACAAGATCAGAGAGGAGAAA 1380
DB 1321 GGGAGATGATGGGGGCTTTAAATTTCCCATGCTAAACAAGATCAGAGAGGAGAAA 1380
QY 1381 GGGCATATGTTTATTTTATATTTTATATTTTCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 GGGCATATGTTTATTTTATATTTTATATTTTCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 AGATCTTCTTCTCTTTTCTGGGTAGAAATTAATCCCGACATTTTATCATCGGTA 1500
DB 1441 AGATCTTCTTCTCTTTTCTGGGTAGAAATTAATCCCGACATTTTATCATCGGTA 1500
QY 1501 GTTTTCTTTCATATTTTGCAAAATGCAAGCTCGTGGGAGCTTTTGTAGTAGA 1560
DB 1501 GTTTTCTTTCATATTTTGCAAAATGCAAGCTCGTGGGAGCTTTTGTAGTAGA 1560
QY 1561 CCATG 1565
DB 1561 CCATG 1565

RESULT 2
US-10-758-799-3
; Sequence 3, Application US/10758799
; Publication No. US20040199944A1
; GENERAL INFORMATION:
; APPLICANT: Dekose, Richard
; Freysinet, Georges
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
; First Intron Of Rice Actin, Chimeric Gene Comprising It
; And Transformed Plant
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```



```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/758, 799
  FILING DATE: 16-Jan-2004
  CLASSIFICATION: 800
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/037, 531
    FILING DATE: 10-MAR-1998
  ATTORNEY/AGENT INFORMATION:
    NAME: McMorrow Jr., Robert G.
    REGISTRATION NUMBER: 30962
    REFERENCE/DOCKET NUMBER: 5500*24
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (302)658-9141
  INFORMATION FOR SEQ ID NO: 3:
    LENGTH: 1565 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
  SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-758-799-3

Query Match      100.0%; Score 1565; DB 19; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCCTGACGAGTCGACGATCCCTTATGACCACTTACTGTATGCAATATCAT 60
DB      1 GAATTCCTGACGAGTCGACGATCCCTTATGACCACTTACTGTATGCAATATCAT 60
QY      61 TTAATGAAATGCAAACTTTCTATCTTCTTACTTACATATCTTGTTTAAAT 120
DB      61 TTAATGAAATGCAAACTTTCTATCTTCTTACTTACATATCTTGTTTAAAT 120
QY      121 TCACTCTCAACATCTTCTCAAGTATGATGAGACCTGTCAAAATTTACTATTTAT 180
DB      121 TCACTCTCAACATCTTCTCAAGTATGATGAGACCTGTCAAAATTTACTATTTAT 180
QY      181 TTCTTCATATTTTTCCTTATACATATTTGGGCTTACATCCATCATATATCA 240
DB      181 TTCTTCATATTTTTCCTTATACATATTTGGGCTTACATCCATCATATATCA 240
QY      241 TCCCTTCCGGTGTCTCTAAAGATTCATCTCTGAATCTTATTCCTTCATAATAGT 300
DB      241 TCCCTTCCGGTGTCTCTAAAGATTCATCTCTGAATCTTATTCCTTCATAATAGT 300
QY      301 TCTCTAAATCAGTCTCTATTAAGCAATCTATATTAAGACATTTTATTTTGTAC 360
DB      301 TCTCTAAATCAGTCTCTATTAAGCAATCTATATTAAGACATTTTATTTTGTAC 360
QY      361 ATATCATTTTGTCTACTCTCAATGCAATTAATATTAATTTTACTTAAACGATAT 420
DB      361 ATATCATTTTGTCTACTCTCAATGCAATTAATATTAATTTTACTTAAACGATAT 420
QY      421 TTAAGATTCAAACGATGAGAACTGTTAGATTAATCTATATTAAGATCCAGT 480
DB      421 TTAAGATTCAAACGATGAGAACTGTTAGATTAATCTATATTAAGATCCAGT 480
QY      481 AGCGTCTCTAAATTTAGATGATTTATTAAGACGCTGTAGAAAACGTAAAAATTC 540
DB      481 AGCGTCTCTAAATTTAGATGATTTATTAAGACGCTGTAGAAAACGTAAAAATTC 540
QY      541 TTGATTTATTTATTTAGGAGTAGAGCTTTATGCTTATTAATCTTTTGTGGAACCA 600
DB      541 TTGATTTATTTATTTAGGAGTAGAGCTTTATGCTTATTAATCTTTTGTGGAACCA 600
QY      601 GCCTTAATACGGATATTTTGCAGATGCGCTCTCATTTTCACTCCAGCGCCCAATTT 660
DB      601 GCCTTAATACGGATATTTTGCAGATGCGCTCTCATTTTCACTCCAGCGCCCAATTT 660
```

```
QY      661 TCAGTTTTTCAACGAGCGCCAGCTGCTACTAACCAAAATTTGATGAGGTGGCGGTT 720
DB      661 TCAGTTTTTCAACGAGCGCCAGCTGCTACTAACCAAAATTTGATGAGGTGGCGGTT 720
QY      721 TTCAAAAGAAATCGAAACCATCTGACCCACCGACTAGTAGGCTCGGATCTTCCCTG 780
DB      721 TTCAAAAGAAATCGAAACCATCTGACCCACCGACTAGTAGGCTCGGATCTTCCCTG 780
QY      781 ATTAAGTCTTAGCAATAGAGCCGCAACCACTTCAAGCGGATGCTGCTTCAAGCTTC 840
DB      781 ATTAAGTCTTAGCAATAGAGCCGCAACCACTTCAAGCGGATGCTGCTTCAAGCTTC 840
QY      841 CACCTATCGGAGCGCGCTCATCTCATCCAAACCTATTCCGTTACCTTCCCATCTCC 900
DB      841 CACCTATCGGAGCGCGCTCATCTCATCCAAACCTATTCCGTTACCTTCCCATCTCC 900
QY      901 GAAAAAATTTCTCGGCTCGGCTCCGACCTTACAAATACCATCCATCCATCAGACGAT 960
DB      901 GAAAAAATTTCTCGGCTCGGCTCCGACCTTACAAATACCATCCATCCATCAGACGAT 960
QY      961 CGCATCACTGCAAAATCCCGCAAGAAATCAACCTCCCAATTCACGCTGCCACCACT 1020
DB      961 CGCATCACTGCAAAATCCCGCAAGAAATCAACCTCCCAATTCACGCTGCCACCACT 1020
QY      1021 CGCGTCTCCCGCGCAAGCAACCAAGAAATTTGGCGCAACCGGATGAGCTCTCCCC 1080
DB      1021 CGCGTCTCCCGCGCAAGCAACCAAGAAATTTGGCGCAACCGGATGAGCTCTCCCC 1080
QY      1081 CTTCCCTCCCGCGCGCGCGGTAACACCCCGCTCTCTCTTCTTCTCCGTTT 1140
DB      1081 CTTCCCTCCCGCGCGCGCGGTAACACCCCGCTCTCTCTTCTTCTCCGTTT 1140
QY      1141 TTTTTCGTCTCGGCTCGATCTTGGGCTTGGATGTTGGGCGAGAGCGGCTTCG 1200
DB      1141 TTTTTCGTCTCGGCTCGATCTTGGGCTTGGATGTTGGGCGAGAGCGGCTTCG 1200
QY      1201 TCGCCCAATCGGTGCGCGGAGAGGCGGATCTCCCGCTGGCGCTCCGGCGTGAAT 1260
DB      1201 TCGCCCAATCGGTGCGCGGAGAGGCGGATCTCCCGCTGGCGCTCCGGCGTGAAT 1260
QY      1261 CGGCGCGGATCTCGCGGGAATGAGGCTCTCGGATGATCTGATCCGCTTGTGG 1320
DB      1261 CGGCGCGGATCTCGCGGGAATGAGGCTCTCGGATGATCTGATCCGCTTGTGG 1320
QY      1321 GGGAGATGATGGGCGTTTAAATTTCCCATCTTAAACCAAGATCAGAAAGGGAATA 1380
DB      1321 GGGAGATGATGGGCGTTTAAATTTCCCATCTTAAACCAAGATCAGAAAGGGAATA 1380
QY      1381 GGGACATATGTTTATTTTATATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB      1381 GGGACATATGTTTATTTTATATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY      1441 AGATCTTCTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1500
DB      1441 AGATCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1500
QY      1501 GTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1560
DB      1501 GTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1560
QY      1561 CCATG 1565
DB      1561 CCATG 1565

RESULT 3
US-09-037-531-1
; Sequence 1, Application US/09037531
; Patent No. US20020104117A1
; GENERAL INFORMATION:
; APPLICANT: Derose, Richard
; APPLICANT: Freysine, Georges
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
```

TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
TITLE OF INVENTION: And Transformed Plant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,531
FILING DATE: 10-MAR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McMorrow Jr., Robert G.
REGISTRATION NUMBER: 30962
REFERENCE/DOCKET NUMBER: 5500*24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)658-9141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1021 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-037-531-1

Query Match 65.2%; Score 1021; DB 9; Length 1021;
Best Local Similarity 100.0%; Pred. No. 9.3e-229;
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 CTTATGCGACCCATTACTGCTAATGCAATCATCATTTATGATGAGCAAACTTTCTATT 86
1 CTTATGCGACCCATTACTGCTAATGCAATCATCATTTATGATGAGCAAACTTTCTATT 60
87 ACTCTTTTACTAATCATATCTGTTTAAATTCAGTCCGCAACATTCATTCCTCAAG 146
61 ACTCTTTTACTAATCATATCTGTTTAAATTCAGTCCGCAACATTCATTCCTCAAG 120
147 TATTAAGTGAAGCTGCAAAATTTACTATTTTATTTCTCATATTTTCTTCTTATACA 206
121 TATTAAGTGAAGCTGCAAAATTTACTATTTTATTTCTCATATTTTCTTCTTATACA 180
207 CATTATGGGCTTACATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 266
181 CATTATGGGCTTACATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 240
267 CCATCTCTGGAATCTTATCTCTCCATATACGTTCTTAATCAGGCTCTTAATGCAAA 326
241 CCATCTCTGGAATCTTATCTCTCCATATACGTTCTTAATCAGGCTCTTAATGCAAA 300
327 TACCTATATTAGAGACATTTTATTTTGTATGATATTTGTCATATCTCTCAATG 386
301 TACCTATATTAGAGACATTTTATTTTGTATGATATTTGTCATATCTCTCAATG 360
387 CATTATACATATTAGTTTACTAATACGATTTTAAAGTATTTCAACGAGGAGGAAGAC 446
361 CATTATACATATTAGTTTACTAATACGATTTTAAAGTATTTCAACGAGGAGGAAGAC 420
447 TGTATGATTAATTTCTATATATAGAGATCCAGTAGCGTCTCTAATTTAGATGATAT 506
421 TGTATGATTAATTTCTATATATAGAGATCCAGTAGCGTCTCTAATTTAGATGATAT 480
507 TTAGAGAGCGCTGTAGAGAAACGTAAGAAATTTCTTGATTAATTTAGGATAGAGT 566
481 TTAGAGAGCGCTGTAGAGAAACGTAAGAAATTTCTTGATTAATTTAGGATAGAGT 540

567 ACCCTTATGCTTATATAGATCTTTGATGAGACCCAGCTTATACCGGTATTTTCCGANT 626
541 ACCCTTATGCTTATATAGATCTTTGATGAGACCCAGCTTATATCCGTTATTTTCCGANT 600
627 GCGCCTTCATTTTCACTTCAGCGCCCAATTTTCAAGTTTCAACCGAAGGCCAGCC 686
601 GCGCCTTCATTTTCACTTCAGCGCCCAATTTTCAAGTTTCAACCGAAGGCCAGCC 660
687 TGCCTTACCAAAATTTGGTATGATGGGCGGTTTCAAAAGATCGGAACCATCTGC 746
661 TGCCTTACCAAAATTTGGTATGATGGGCGGTTTCAAAAGATCGGAACCATCTGC 720
747 ACCCAACGACTGTAGGCGCTCGATTCCTCTGATTAAGTCTTACCAATAGAGACCA 806
721 ACCCAACGACTGTAGGCGCTCGATTCCTCTGATTAAGTCTTACCAATAGAGACCA 780
807 GAACCAACCATGAGCGGATGCTCTTCAAGCTTCACTCATGCGCGCTCATCTCCA 866
781 GAACCAACCATGAGCGGATGCTCTTCAAGCTTCACTCATGCGCGCTCATCTCCA 840
867 TCCACACCTATTCGTTACCTTGCCTCCGAAATTTCTCGGCTGCGCTCGCC 926
841 TCCACACCTATTCGTTACCTTGCCTCCGAAATTTCTCGGCTGCGCTCGCC 900
927 ACTCTAATTAATCAATCCATCCATGACGAGCATGCACTGACCAATTCGCCAGAA 986
901 ACTCTAATTAATCAATCCATCCATGACGAGCATGCACTGACCAATTCGCCAGAA 960
987 ATCAACACCTCCCAATTCACGCTGCAACCACTGCGCTCTCCGCGCAAGCAACAA 1046
961 ATCAACACCTCCCAATTCACGCTGCAACCACTGCGCTCTCCGCGCAAGCAACAA 1020
1047 G 1047
1021 G 1021

RESULT 4
US-10-758-799-1
Sequence 1, Application US/10758799
Publication No. US2004019944A1
GENERAL INFORMATION:
APPLICANT: Derose, Richard
Freysinet, Georges
TITLE OF INVENTION: Maize H3CA Promoter Combined With The
First Intron Of Rice Actin, Chimeric Gene Comprising It
And Transformed Plant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/758,799
FILING DATE: 16-Jan-2004
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/037,531
FILING DATE: 10-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: McMorrow Jr., Robert G.
REGISTRATION NUMBER: 30962
REFERENCE/DOCKET NUMBER: 5500*24
TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 658-9141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1021 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-758-799-1

Query Match 65.2%; Score 1021; DB 19; Length 1021;
Best Local Similarity 100.0%; Pred. No. 9.3e-229;
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CTTATGTGACCACTTACTGTAAATGATATCATTTTAAATGATAGCAAACTTTCTATT 86
DB 1 CTTATGTGACCACTTACTGTAAATGATATCATTTTAAATGATAGCAAACTTTCTATT 60
QY 87 ACTTCTTTACTTAACATTAATCTTGGTTTAAATTCAGTCTTCAACATTCATTGCTCAG 146
DB 61 ACTTCTTTACTTAACATTAATCTTGGTTTAAATTCAGTCTTCAACATTCATTGCTCAG 120
QY 147 TATAGTGTGACGCTGCAAAATTTACTATTATTTCTCATATTTTTCCTTATACA 206
DB 121 TATAGTGTGACGCTGCAAAATTTACTATTATTTCTCATATTTTTCCTTATACA 180
QY 207 CATTTTGGGCTTACATTCATCATCTATATCCATCTTCCGCTGCTCTTAAAGATT 266
DB 181 CATTTTGGGCTTACATTCATCATCTATATCCATCTTCCGCTGCTCTTAAAGATT 240
QY 267 CCATCTCTGATCTTATCTCTCCAAATACGTTCTTAAATCAGTCTCTTAAAGCA 326
DB 241 CCATCTCTGATCTTATCTCTCCAAATACGTTCTTAAATCAGTCTCTTAAAGCA 300
QY 327 TACCTATATAGAGACATTTTATTTTGTATCATATCATTTTGTATATCTTCAAGT 386
DB 301 TACCTATATAGAGACATTTTATTTTGTATCATATCATTTTGTATATCTTCAAGT 360
QY 387 CATTAATCATATTTAGTTTACTTAAACGATTTTAAATTTTAAATTTTAAACGATGAGAAC 446
DB 361 CATTAATCATATTTAGTTTACTTAAACGATTTTAAATTTTAAATTTTAAACGATGAGAAC 420
QY 447 TGTATAGATTAATCTATATATAGAGATCCAGTAGCGTTCTTAAATTTAGATGATT 506
DB 421 TGTATAGATTAATCTATATATAGAGATCCAGTAGCGTTCTTAAATTTAGATGATT 480
QY 507 TTAGAGAGCGCTGTAGAAAACGTAATAATCTTTGATATTTATTTAGGGTAGAGT 566
DB 481 TTAGAGAGCGCTGTAGAAAACGTAATAATCTTTGATATTTATTTAGGGTAGAGT 540
QY 567 AGCCTTATAGCTTATATGATCTTTGGGACCCAGCTTATACCGGTTATTTTCCGAGTT 626
DB 541 AGCCTTATATCTTATATGATCTTTGGGACCCAGCTTATACCGGTTATTTTCCGAGTT 600
QY 627 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCAAGTTTTCACCGGAACGCGCCAGCC 686
DB 601 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCAAGTTTTCACCGGAACGCGCCAGCC 660
QY 687 TGGCTTAACCAAAATTTGTAGCGGTGGCGGTTTCAAAAAGAGTGGGAAACATCTGCG 746
DB 661 TGGCTTAACCAAAATTTGTAGCGGTGGCGGTTTCAAAAAGAGTGGGAAACATCTGCG 720
QY 747 ACCCAACGCTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTAGGCAATAGAGGCCA 806
DB 721 ACCCAACGCTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTAGGCAATAGAGGCCA 780
QY 807 GAACCAACGCTAGTAGGCGGTGCTCTAGCGTTTCAACCTCATGCGCGCGCTCATCTCCA 866
DB 781 GAACCAACGCTAGTAGGCGGTGCTCTAGCGTTTCAACCTCATGCGCGCGCTCATCTCCA 840
QY 867 TCAACACGCTATTCGCTTACCTTGGCCATCTCCGAAAAAATTTCTGGGCTCGGCGTCCG 926

DB 841 TCAACACGCTATTCGCTTACCTTGGCCATCTCCGAAAAAATTTCTGGGCTCGGCTCCG 900
QY 927 ACTTACTACAAATATCCATTCCTCATCGACGCGATGCTATCTGCGCAATTCGCCAGAA 986
DB 901 ACTTACTACAAATATCCATTCCTCATCGACGCGATGCTATCTGCGCAATTCGCCAGAA 960
QY 987 ATCAACACGCTCCCAATTTCCAGCGTGGCACCAACTGCGCGTCTCGGCGCAAGCAACAA 1046
DB 961 ATCAACACGCTCCCAATTTCCAGCGTGGCACCAACTGCGCGTCTCGGCGCAAGCAACAA 1020
QY 1047 G 1047
DB 1021 G 1021

RESULT 5
US-09-037-531-2
; Sequence 2, Application US/09037531
; Patent No. US20020104117A1
; GENERAL INFORMATION:
; APPLICANT: Dekose, Richard
; TITLE OF INVENTION: Freysinet, Georges
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
; TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,531
; FILING DATE: 10-MAR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G.
; REGISTRATION NUMBER: 30962
; REFERENCE/DOCKET NUMBER: 5500*24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-037-531-2

Query Match 29.0%; Score 454; DB 9; Length 454;
Best Local Similarity 100.0%; Pred. No. 4.9e-96;
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1102 GTAACACCCCGCCCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1161
DB 1 GTAACACCCCGCCCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 60
QY 1162 CTTTGGCTTTGGATTTGGGTTGGGAGAGGCGCTTCTGTCGCGCCAGATCGGTCGCGG 1221
DB 61 CTTTGGCTTTGGATTTGGGTTGGGAGAGGCGCTTCTGTCGCGCCAGATCGGTCGCGG 120
QY 1222 AGGGGCGGATCTCGGCGTGGGCTTCCGCGGTGAGTCCGCGCGGATCTTCCGCGGGA 1281
DB 121 AGGGGCGGATCTCGGCGTGGGCTTCCGCGGTGAGTCCGCGCGGATCTTCCGCGGGA 180

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 04:01:02 : Search time 5357.74 Seconds
(without alignments)
14153.802 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565
Sequence: 1 GAATTCCTGACGATCGACG.....TTTTTGTAGTAGACCATG 1565

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenBml:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1565	100.0	1565	6 A94725	A94725 Sequence 3
2	1565	100.0	1565	6 AR559745	AR559745 Sequence
3	1565	100.0	1565	6 BD128391	BD128391 Corn H3C4
4	1021	65.2	1021	6 A94723	A94723 Sequence 1
5	1021	65.2	1021	6 AR559743	AR559743 Sequence
6	1021	65.2	1021	6 BD128389	BD128389 Corn H3C4
7	454	29.0	454	6 A94724	A94724 Sequence 2
8	454	29.0	454	6 AR559744	AR559744 Sequence
9	454	29.0	454	6 BD128390	BD128390 Corn H3C4
10	400	25.6	1264	6 MZEH3C4	MZEH3C4 Maize (Zea
11	296	18.9	623	6 AX467609	AX467609 Sequence
12	296	18.9	623	8 OSACT1	OSACT1 O. sativa Ac
13	296	18.9	1392	6 IS0114	IS0114 Sequence 6
14	296	18.9	1404	6 IS0115	IS0115 Sequence 6
15	296	18.9	2199	6 IS0113	IS0113 Sequence 5
16	296	18.9	5643	6 IS0112	IS0112 Sequence 4
17	294	18.8	470	6 AX55357	AX55357 Sequence
18	237	15.1	4895	12 AY452735	AY452735 Reporter
19	236	15.1	1266	8 S44221	S44221 Act1=actin

20	236	15.1	4412	12 EVCOR112N	Z29587 Expression
21	236	15.1	4433	12 EVCOR11AN	Z29588 Expression
22	236	15.1	4466	12 EVCOR116N	Z29589 Expression
23	210	13.4	1121	6 AX641982	AX641982 Sequence
24	145	9.3	4032	6 A71435	A71435 Sequence 5
25	145	9.3	4032	6 AR207453	AR207453 Sequence
26	145	9.3	4032	6 AR564463	AR564463 Sequence
27	145	9.3	4032	6 BD065609	BD065609 Improved
28	145	9.3	7545	6 AX840288	AX840288 Sequence
29	145	9.3	7943	6 AX093010	AX093010 Sequence
30	145	9.3	9143	6 AX093007	AX093007 Sequence
31	145	9.3	10003	6 AX093016	AX093016 Sequence
32	145	9.3	11643	6 AX840289	AX840289 Sequence
33	142	9.1	9359	6 AX384394	AX384394 Sequence
34	142	9.1	9359	6 AX473364	AX473364 Sequence
35	141	9.0	2318	6 BD014494	BD014494 Transgen
36	141	9.0	6865	6 AX093008	AX093008 Sequence
37	141	9.0	10003	6 AX093016	AX093016 Sequence
38	141	9.0	13474	12 AY252519	AY252519 Cloning v
39	141	9.0	13485	12 AY252520	AY252520 Cloning v
40	140	8.9	3039	6 AR271021	AR271021 Sequence
41	140	8.9	3039	6 AR271022	AR271022 Sequence
42	140	8.9	3044	6 AR271033	AR271033 Sequence
43	140	8.9	3450	6 AR271020	AR271020 Sequence
44	140	8.9	3455	6 AR271032	AR271032 Sequence
45	140	8.9	3469	6 AR271023	AR271023 Sequence

ALIGNMENTS

RESULT 1
A94725
LOCUS A94725 1565 bp DNA linear PAT 26-JUN-2000
DEFINITION Sequence 3 from Patent WO9934005.
ACCESSION A94725
VERSION A94725.1 GI:6778990
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1565)
AUTHORS Derose,R. and Freysinet,G.
TITLE MAIZE H3C4 PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON,
JOURNAL CHIMERIC GENE CONTAINING IT AND TRANSFORMED PLANT
Patent: WO 9934005-A 3 08-JUL-1999;
FEATURES
source
1..1565
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
27..1047
1102..1555
ORIGIN
promoter
intron
Query Match 100.0%; Score 1565; DB 6; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 TTTCTCATATTTTTTTTCTTATACATTTTGGGCTTACATTCATCTATATCCA 240
Qy 241 TCCCTTCCGGTGTCTCTAAAGATTCATCTCTGAATCTTATCTCTCCAAATACGT 300
Db 241 TCCCTTCCGGTGTCTCTAAAGATTCATCTCTGAATCTTATCTCTCCAAATACGT 300
Qy 301 TCTCTAAATCAGGCTCTATAGCAATACCTATATTAGACATTTTATTTTGTGTAC 360
Db 301 TCTCTAAATCAGGCTCTATAGCAATACCTATATTAGACATTTTATTTTGTGTAC 360
Qy 361 ATACATATTTGTCACTCTCAATGCAATATATATTAGTTTATTAACCAATAT 420
Db 361 ATACATATTTGTCACTCTCAATGCAATATATATTAGTTTATTAACCAATAT 420
Qy 421 TTTAAAGTATCAACCGATGAAAGACTTTAGATTAATCTTATATAGAAATCAGT 480
Db 421 TTTAAAGTATCAACCGATGAAAGACTTTAGATTAATCTTATATAGAAATCAGT 480
Qy 481 AGGCTTCTTAAATTTAGATGATTTATAGAGACGCTTTAGAAAACTTAAATTTCT 540
Db 481 AGGCTTCTTAAATTTAGATGATTTATTTAGAGACGCTTTAGAAAACTTAAATTTCT 540
Qy 541 TTGATTATTTATATTTAGGATGAGTAGACCTTTATGCTTTATAGATCTTTGTGACCA 600
Db 541 TTGATTATTTATATTTAGGATGAGTAGACCTTTATGCTTTATAGATCTTTGTGACCA 600
Qy 601 GCCTTATACCGGTTATTTTGGCAATGCGGCTCTCATTTTCACTCCAGCCCACTTT 660
Db 601 GCCTTATACCGGTTATTTTGGCAATGCGGCTCTCATTTTCACTCCAGCCCACTTT 660
Qy 661 TCAAGTTTTCACGGAAGCGCCAGCCTGACCTTAACCAATTTGTAGGATGAGGAGT 720
Db 661 TCAAGTTTTCACGGAAGCGCCAGCCTGACCTTAACCAATTTGTAGGATGAGGAGT 720
Qy 721 TTCAAAAGAAATCGAAACCATCTGCAACCAACGACTAGTAGGAGCTTCGCTCTG 780
Db 721 TTCAAAAGAAATCGAAACCATCTGCAACCAACGACTAGTAGGAGCTTCGCTCTG 780
Qy 781 ATTAAAGTCTTAGCCAAATAGAGCCAGAACCAACCATGAGGAGTGTCTTACGCTTC 840
Db 781 ATTAAAGTCTTAGCCAAATAGAGCCAGAACCAACCATGAGGAGTGTCTTACGCTTC 840
Qy 841 CACCTCATCGGCGCGGCTGCACTTCATCCATCAACCTTATGCTTACCTTCCATCTCC 900
Db 841 CACCTCATCGGCGCGGCTGCACTTCATCCATCAACCTTATGCTTACCTTCCATCTCC 900
Qy 901 GAAAAAATTTCTCGGCTGCGCTCGCACTCTACTCAAAATACCAATCCATCACGAGCAT 960
Db 901 GAAAAAATTTCTCGGCTGCGCTCGCACTCTACTCAAAATACCAATCCATCACGAGCAT 960
Qy 961 CGCATCACTGCAATCCCCCAAAATCAACACTCTCCAAATTCACAGCTGCCACAAT 1020
Db 961 CGCATCACTGCAATCCCCCAAAATCAACACTCTCCAAATTCACAGCTGCCACAAT 1020
Qy 1021 CGCGCTCTCGGCGCAAGAACCAAGAAATTTGGCGGCAACCGGAGGAGGAGTCTCTCC 1080
Db 1021 CGCGCTCTCGGCGCAAGAACCAAGAAATTTGGCGGCAACCGGAGGAGGAGTCTCTCC 1080
Qy 1081 CTTCCCTCTCGCGCGCGGCTGTAACCAACCCGCTCTCTCTTTCTTTCTCGTTTT 1140
Db 1081 CTTCCCTCTCGCGCGCGGCTGTAACCAACCCGCTCTCTCTTTCTTTCTCGTTTT 1140
Qy 1141 TTTTTCCTGCTCGGCTCTGCAATCTTTGGCTTTGGATTTGGGATGGGAGAGGAGTCTG 1200
Db 1141 TTTTTCCTGCTCGGCTCTGCAATCTTTGGCTTTGGATTTGGGATGGGAGAGGAGTCTG 1200
Qy 1201 TCGGCAAGATCGGATCGGAGAGGAGGAGGAGTCTCGGAGTGTGAGATCCGCGGTGTGG 1260
Db 1201 TCGGCAAGATCGGATCGGAGAGGAGGAGGAGTCTCGGAGTGTGAGATCCGCGGTGTGG 1260
Qy 1261 CGGCGCGGATCTCTCGCGGAGATGAGGCTCTCGGATGTAGATCCGCGGTGTGG 1320
Db 1261 CGGCGCGGATCTCTCGCGGAGATGAGGCTCTCGGATGTAGATCCGCGGTGTGG 1320

Db 1261 CGGCGCGGATCTCTCGGAGAGTGGGAGTGTGAGATGTGATCCGCGGTGTGG 1320
Qy 1321 GGGAGATGATGGGGGTTTAAATTTCCGCAATGCTAAACAAATGCAAGAGAGGAGAAA 1380
Db 1321 GGGAGATGATGGGGGTTTAAATTTCCGCAATGCTAAACAAATGCAAGAGAGGAGAAA 1380
Qy 1381 GGGCACTATGTTTATTTTATTTATTTATTTTCTGCTGCTGCTGAGGCTTATGATGCT 1440
Db 1381 GGGCACTATGTTTATTTTATTTATTTATTTTCTGCTGCTGCTGAGGCTTATGATGCT 1440
Qy 1441 AGATCTTCTTCTTCTTCTTCTTGTGGTAGAATTTGAATCCCTCAGCATTTGTCATCGTA 1500
Db 1441 AGATCTTCTTCTTCTTCTTGTGGTAGAATTTGAATCCCTCAGCATTTGTCATCGTA 1500
Qy 1501 GTTTTCTTTTATGATTTTGTGACAAATGACGCTCGAGGAGCTTTTGTAGGTAGA 1560
Db 1501 GTTTTCTTTTATGATTTTGTGACAAATGACGCTCGAGGAGCTTTTGTAGGTAGA 1560
Qy 1561 CCATG 1565
Db 1561 CCATG 1565

RESULT 2
AR559745 1565 bp DNA linear PAT 08-OCT-2004
LOCUS AR559745
DEFINITION Sequence 3 from patent US 6750378.
ACCESSION AR559745
VERSION AR559745.1 GI:53969843
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1565)
AUTHORS Derose, R. and Freysinet, G.
TITLE Maize H3C4 promoter combined with the first intron of rice actin, chimeric gene comprising it and transformed plant
JOURNAL Patent: US 6750378-A 3 15-JUN-2004;
FEATURES
source 1..1565
/organism="Unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 1565; DB 6; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATTCCTGCAAGTGCAGGATCCCTTATGTGACCACTTATCTGTAAATGATATCAT 60
Db 1 GAATTCCTGCAAGTGCAGGATCCCTTATGTGACCACTTATCTGTAAATGATATCAT 60
Qy 61 TTAATGAATPAGCAAACTTTTCTTATTTACTTTTACTTAACATTAATCTTGGTTTAAAT 120
Db 61 TTAATGAATPAGCAAACTTTTCTTATTTACTTTTACTTAACATTAATCTTGGTTTAAAT 120
Qy 121 TCAGTCTCAACATTCATGCTCAAGTATAGTGAAGTGAAGTCAAAATTTACTATTTTAT 180
Db 121 TCAGTCTCAACATTCATGCTCAAGTATAGTGAAGTGAAGTCAAAATTTACTATTTTAT 180
Qy 181 TTTCTCATATTTTTTTTCTTATACATTTTGGGCTTACATTCATCATCATATATCCA 240
Db 181 TTTCTCATATTTTTTTTCTTATACATTTTGGGCTTACATTCATCATCATATATCCA 240
Qy 241 TCTTTTCCGGTGTCTCTAAAGATTCATCTCTGAATCTTATCTCTCCAAATACGT 300
Db 241 TCTTTTCCGGTGTCTCTAAAGATTCATCTCTGAATCTTATCTCTCCAAATACGT 300
Qy 301 TCTCTAAATCAGGCTCTATAGCAATACCTATATTAGACATTTTATTTTGTGTAC 360
Db 301 TCTCTAAATCAGGCTCTATAGCAATACCTATATTAGACATTTTATTTTGTGTAC 360
Qy 361 ATACATATTTGTCACTCTCAATGCAATATATATTAGTTTATTAACCAATAT 420
Db 361 ATACATATTTGTCACTCTCAATGCAATATATATTAGTTTATTAACCAATAT 420

Db	241	TCCTTTCCGGTGTCTCTAAAAGATTCATCTCTGAATCTTATTCCTCCAAATACGT	300
Qy	301	TCCTCAAATCAGGTCCTCTATAAGCAATACCTATAATTAGACATTTTATTTTGTAC	360
Db	301	TCTCTAATACAGGTCCTCTATAAGCAATACCTATAATTAGACATTTTATTTTGTAC	360
Qy	361	ATACATATTGTCTATCTCTCAATGCATTTATACATATTAGTTTACTAAACGATAT	420
Db	361	ATACATATTGTCTATCTCTCAATGCATTTATACATATTAGTTTACTAAACGATAT	420
Qy	421	TTAAAGTATTCAAACGATGAAAGACGTATTAGATTAATTCCTATATATAGAAATCCAGT	480
Db	421	TTAAAGTATTCAAACGATGAAAGACGTATTAGATTAATTCCTATATATAGAAATCCAGT	480
Qy	481	AGCGTCTCTAAATTTAGATGATTTATTTAGAGAGACGCTGTAGAAACGTAAAAATTC	540
Db	481	AGCGTCTCTAAATTTAGATGATTTATTTAGAGAGACGCTGTAGAAACGTAAAAATTC	540
Qy	541	TTGATTTATTTATTTAGGGTAGAGTAGCCTTTATATGCTTTATATAGCTTTGTGAGACCA	600
Db	541	TTGATTTATTTATTTAGGGTAGAGTAGCCTTTATATGCTTTATATAGCTTTGTGAGACCA	600
Qy	601	GCGTTATACCGGTTATTTTGGGATTTGGCCCTCATTTTCACTCGAGGCCCAATTT	660
Db	601	GCGTTATACCGGTTATTTTGGGATTTGGCCCTCATTTTCACTCGAGGCCCAATTT	660
Qy	661	TCACGTTTTCACCGAAGCGCCAGCCTCCTTAACCAACAAATTTGGTACGATGGCGGTT	720
Db	661	TCACGTTTTCACCGAAGCGCCAGCCTCCTCATCAACCAAAATTTGGTACGATGGCGGTT	720
Qy	721	TTCAAAAGAAGTCGGAACCAATCTTGACCCACCGATAGTAGGCCCTCGATCTCCCTG	780
Db	721	TTCAAAAGAAGTCGGAACCAATCTTGACCCACCGATAGTAGGCCCTCGATCTCCCTG	780
Qy	781	ATTAGTCTCTAGCCCAATAGAGCCCGAACAACCATACCGGATTCGCTCCCTACGCTTC	840
Db	781	ATTAGTCTCTAGCCCAATAGAGCCCGAACAACCATACCGGATTCGCTCCCTACGCTTC	840
Qy	841	CACCTCATCGGCGCGCTCATCTCCATCTCAACACCTATTCGTTACCTTGGCCATCTCC	900
Db	841	CACCTCATCGGCGCGCTCATCTCCATCTCAACACCTATTCGTTACCTTGGCCATCTCC	900
Qy	901	GAATAAAATTCCTGCGCTCGCGCTCGGCACCTTACCAAAATTCATCCATCGACGAT	960
Db	901	GAATAAAATTCCTGCGCTCGCGCTCGGCACCTTACCAAAATTCATCCATCGACGAT	960
Qy	961	CGCATCATCTGCCAATTCCTCCAGAAATTCACACTCCCAATTCACGCTGACCAACT	1020
Db	961	CGCATCATCTGCCAATTCCTCCAGAAATTCACACTCCCAATTCACGCTGACCAACT	1020
Qy	1021	CGCGTCTCTCGCGCGCGCAAGACCAAAAGAAATTGGCGGACACCGCGGTGGAAGCTCCTCCC	1080
Db	1021	CGCGTCTCTCGCGCGCGCAAGACCAAAAGAAATTGGCGGACACCGCGGTGGAAGCTCCTCCC	1080
Qy	1081	CCTCCCTCTCGCGCGCGCGGTAAACAACCCCGCCCTCTCCTCTTTCTTCGCTTT	1140
Db	1081	CCTCCCTCTCGCGCGCGCGGTAAACAACCCCGCCCTCTCCTCTTTCTTCGCTTT	1140
Qy	1141	TTTTTTTGGTCTCGGTCTGATCTTTGGCCTTGGTATGTTGGGTGGGCAAGCGGCTTGG	1200
Db	1141	TTTTTTTGGTCTCGGTCTGATCTTTGGCCTTGGTATGTTGGGTGGGCAAGCGGCTTGG	1200
Qy	1201	TGCGCCAGATCGGATCGCGGGAAGGGGCGGAATCTGCGGCTGGCGCTCCGGAAGTAGAT	1260
Db	1201	TGCGCCAGATCGGATCGCGGGAAGGGGCGGAATCTGCGGCTGGCGCTCCGGAAGTAGAT	1260
Qy	1261	CGGCCCGGATCTCTCGCGGGGAATGGGGCTTCTCGATGTATGATCTGATCCGCGGTTGG	1320
Db	1261	CGGCCCGGATCTCTCGCGGGGAATGGGGCTTCTCGATGTATGATCTGATCCGCGGTTGG	1320
Qy	1321	GGGAGATGATGGGCGTTTAAAAATTTCCGATGCTAAACAGATCAGAAAGGGGAAAA	1380

Db	1321	GGGAGATGATGGGGCGTTTAAAAATTTGGCCATGCTAAACAAGATCAGAAAGGGGAAAA	1380
Qy	1381	GGGCACTATGATTATAATTTTATATAATTTCTGCTGCTGCTCGTCAAGCTTAGATGTC	1440
Db	1381	GGGCACTATGATTATAATTTTATAATTTCTGCTGCTGCTCGTCAAGCTTAGATGTC	1440
Qy	1441	AGATCTTCTCTCTCTCTTTTGGGGGATGAATTTGAATCCCTGACGATGTCATCGGTA	1500
Db	1441	AGATCTTCTCTCTCTCTTTTGGGGGATGAATTTGAATCCCTGACGATGTCATCGGTA	1500
Qy	1501	GTTCCTTTTTCATGATTTTGACAAATGACGCTCGTGGGAGCTTTTGTAGTAGA	1560
Db	1501	GTTCCTTTTTCATGATTTTGACAAATGACGCTCGTGGGAGCTTTTGTAGTAGA	1560
Qy	1561	CCATG 1565	
Db	1561	CCATG 1565	
RESULT 4			
A94723		1021 bp	DNA
LOCUS	A94723		linear
DEFINITION	Sequence 1 from Patent WO934005.		PAT 26-JAN-2000
ACCESSION	A94723		
VERSION	A94723.1		GI:6778988
KEYWORDS			
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 1021)		
AUTHORS	Derose,R. and Freyasiniet,G.		
TITLE	MAIZE H3Gc PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON, CHMERIC GENE CONTAINING IT AND TRANSFORMED PLANT Patent: WO 934005-A 1 08-JUL-1993;		
JOURNAL	PHONE POLULENT AGROCHIMIE (FR)		
FEATURES	location/Qualifiers		
source	1..1021		
ORIGIN	/organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"		
Promoter	1..1021		
Query Match	65.2%; Score 1021; DB 6; Length 1021;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 1021; Conservative	0; Mismatches	0; Indels	0; Gaps
Qy	27	CTTATGCGACATTTACTGTAAATGCAATTCATTTAATGAATGCAAACTTTCTATT	86
Db	1	CTTATGCGACATTTACTGTAAATGCAATTCATTTAATGAATGCAAACTTTCTATT	60
Qy	87	ACTCTTTACTACATATAATCTTGTTTAAATTAATCACTCCTCAACATTCATTCCTCAAG	146
Db	61	ACTCTTTACTACATATAATCTTGTTTAAATTAATCACTCCTCAACATTCATTCCTCAAG	120
Qy	147	TATAAGTTAGACTGTCAAAAATTTACTATATTTTCTCATATTTTCTTATACA	206
Db	121	TATAAGTTAGACTGTCAAAAATTTACTATATTTTCTCATATTTTCTTATACA	180
Qy	207	CATTTTGGGCTTACATCCATCATCTATATCCATCCTTCCGGTGTCTTAAGATT	266
Db	181	CATTTTGGGCTTACATCCATCATCTATATCCATCCTTCCGGTGTCTTAAGATT	240
Qy	267	CCATCCTGTGAATCTTATTCCTCCAAATAAGTTCTTAATAGGCTCTTATAGCAA	326
Db	241	CCATCCTGTGAATCTTATTCCTCCAAATAAGTTCTTAAATAGGCTCTTATAGCAA	300
Qy	327	TACCTATATTAAGACATTTTATAATTTTGTACATACATATTTGTCACTCTCAATG	386
Db	301	TACCTATATTAAGACATTTTATAATTTTGTACATACATATTTGTCACTCTCAATG	360
Qy	387	CATTTATCATTTTATAGTTTACTTAACGATTAATTTAAAGTATCAACCGATGAAGAC	446

Db 361 CATTATACATATTAGTTTACTAAACCGATTAATTAAAGTATTCAAACGATGAAGAAC 420
 QY 447 TGTTCATATTAATTCATATATATAGAGATCCAGTACGCTTCTAAATTTAGATGATTAT 506
 Db 421 TGTTCATATTAATTCATATATATAGAGATCCAGTACGCTTCTAAATTTAGATGATTAT 480
 QY 507 TTGAGAGACGCTGTAGAGAAACGTAATAATTCCTTGAATTATTTAGAGGTAGT 566
 Db 481 TTGAGAGACGCTGTAGAGAAACGTAATAATTCCTTGAATTATTTAGAGGTAGT 540
 QY 567 AGCTTTATATCTTATATAGATCTTTGGTGAACCCAGCTTATACCGGTTATTTTGCAGTT 626
 Db 541 AGCTTTATATCTTATATAGATCTTTGGTGAACCCAGCTTATACCGGTTATTTTGCAGTT 600
 QY 627 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCAAGTTTTCACGAAACGCCAGCC 686
 Db 601 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCAAGTTTTCACGAAACGCCAGCC 660
 QY 687 TGCCTAACCAAAATTTGTACGCTGGCGGGTTTCAAAAAGAGTCGGAACCATCTGC 746
 Db 661 TGCCTAACCAAAATTTGTACGCTGGCGGGTTTCAAAAAGAGTCGGAACCATCTGC 720
 QY 747 ACCACCGACTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTAGGCAATAGAGGCCA 806
 Db 721 ACCACCGACTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTAGGCAATAGAGGCCA 780
 QY 807 GAACCAACCATCAACGCGGATCGTCCCTTCAAGCTTCACTCATCGCGCGCTCAATCTCA 866
 Db 781 GAACCAACCATCAACGCGGATCGTCCCTTCAAGCTTCACTCATCGCGCGCTCAATCTCA 840
 QY 867 TCCAAACCTTATTCCTGTTACCTTGGCCATCTCTCGAAAAAATTTCTCGGCTCGGCTCCG 926
 Db 841 TCCAAACCTTATTCCTGTTACCTTGGCCATCTCTCGAAAAAATTTCTCGGCTCGGCTCCG 900
 QY 927 ACCCTACCAAAATACCATCCATCCATCAGACGATCGATCACTGCCAAATCCCCAGAA 986
 Db 901 ACCCTACCAAAATACCATCCATCCATCAGACGATCGATCACTGCCAAATCCCCAGAA 960
 QY 987 ATCAACACTCCCAATTCACGCTGCCACCAACTCGCGCTCTCCGCGCAAGACCAAA 1046
 Db 961 ATCAACACTCCCAATTCACGCTGCCACCAACTCGCGCTCTCCGCGCAAGACCAAA 1020
 QY 1047 G 1047
 Db 1021 G 1021

RESULT 5
 AR559743
 LOCUS AR559743 1021 bp DNA linear PAT 08-OCT-2004
 DEFINITION Sequence 1 from patent US 6750378.
 ACCESSION AR559743
 VERSION AR559743.1 GI:53969841
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 AUTHORS 1 (bases 1 to 1021)
 TITLE Derose R. and Freyresinet G.
 JOURNAL Maize H3c4 promoter combined with the first intron of rice actin,
 FEATURES chimERIC gene comprising it and transformed plant
 Patent: US 6750378-A 1 15-JUN-2004;
 Location/Qualifiers
 1..1021
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 65.2%; Score 1021; DB 6; Length 1021;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CTTATGCAACATTTACTGTAATGCAATATCAATTATTAATGAATAGCAAACTTTCTATT 86

Db 1 CTTATGCAACATTTACTGTAATGCAATATCAATTATTAATGAATAGCAAACTTTCTATT 60
 QY 87 ACTTCCTTAACATTAATTCCTGTTTAAATTCAGTCTCCACATTCATGCTCAAG 146
 Db 61 ACTTCCTTAACATTAATTCCTGTTTAAATTCAGTCTCCACATTCATGCTCAAG 120
 QY 147 TATTAATGAGACTGCAAAATTTACTATTTATTTCTCATATTTTCTTCTTATACA 206
 Db 121 TATTAATGAGACTGCAAAATTTACTATTTATTTCTCATATTTTCTTCTTATACA 180
 QY 207 CATTGGGCGCTTACATCATCATCATATATCCATCTTCCGCTGCTCAAAAGATT 266
 Db 181 CATTGGGCGCTTACATCATCATCATATATCCATCTTCCGCTGCTCAAAAGATT 240
 QY 267 CCATCCTGTAATCTTATTCCTCCATTAACGTTCTTAATCAGTCTCATTAAGCA 326
 Db 241 CCATCCTGTAATCTTATTCCTCCATTAACGTTCTTAATCAGTCTCATTAAGCA 300
 QY 327 TACCTTATTAAGAGACATTTTATTTTGTATACATATTTTGTATATCTCAATG 386
 Db 301 TACCTTATTAAGAGACATTTTATTTTGTATACATATTTTGTATATCTCAATG 360
 QY 387 CATTATACATTTATTTAGTTTATCTTAACCGATTAATTAAAGTATTCAAACGATGAAGAAC 446
 Db 361 CATTATACATTTATTTAGTTTATCTTAACCGATTAATTAAAGTATTCAAACGATGAAGAAC 420
 QY 447 TGTTCATATTAATTCATATATATAGAGATCCAGTACGCTTCTAAATTTAGATGATTAT 506
 Db 421 TGTTCATATTAATTCATATATATAGAGATCCAGTACGCTTCTAAATTTAGATGATTAT 480
 QY 507 TTGAGAGACGCTGTAGAGAAACGTAATAATTCCTTGAATTATTTAGAGGTAGT 566
 Db 481 TTGAGAGACGCTGTAGAGAAACGTAATAATTCCTTGAATTATTTAGAGGTAGT 540
 QY 567 AGCTTTATATCTTATATAGATCTTTGGTGAACCCAGCTTATACCGGTTATTTTGCAGTT 626
 Db 541 AGCTTTATATCTTATATAGATCTTTGGTGAACCCAGCTTATACCGGTTATTTTGCAGTT 600
 QY 627 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCAAGTTTTCACGAAACGCCAGCC 686
 Db 601 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCAAGTTTTCACGAAACGCCAGCC 660
 QY 687 TGCCTAACCAAAATTTGTACGCTGGCGGGTTTCAAAAAGAGTCGGAACCATCTGC 746
 Db 661 TGCCTAACCAAAATTTGTACGCTGGCGGGTTTCAAAAAGAGTCGGAACCATCTGC 720
 QY 747 ACCACCGACTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTAGGCAATAGAGGCCA 806
 Db 721 ACCACCGACTAGTAGGCGCTCGGATCTCTCGATTAAGTCTTAGGCAATAGAGGCCA 780
 QY 807 GAACCAACCATCAACGCGGATCGTCCCTTCAAGCTTCACTCATCGCGCGCTCAATCTCA 866
 Db 781 GAACCAACCATCAACGCGGATCGTCCCTTCAAGCTTCACTCATCGCGCGCTCAATCTCA 840
 QY 867 TCCAAACCTTATTCCTGTTACCTTGGCCATCTCTCGAAAAAATTTCTCGGCTCGGCTCCG 926
 Db 841 TCCAAACCTTATTCCTGTTACCTTGGCCATCTCTCGAAAAAATTTCTCGGCTCGGCTCCG 900
 QY 927 ACCCTACCAAAATACCATCCATCCATCAGACGATCGATCACTGCCAAATCCCCAGAA 986
 Db 901 ACCCTACCAAAATACCATCCATCCATCAGACGATCGATCACTGCCAAATCCCCAGAA 960
 QY 987 ATCAACACTCCCAATTCACGCTGCCACCAACTCGCGCTCTCCGCGCAAGACCAAA 1046
 Db 961 ATCAACACTCCCAATTCACGCTGCCACCAACTCGCGCTCTCCGCGCAAGACCAAA 1020
 QY 1047 G 1047
 Db 1021 G 1021

RESULT 6

BD128389 1021 bp DNA linear PAT 18-SEP-2002
LOCUS BD128389
DEFINITION Corn H3c4 promoter bonded to the first intron of rice actin,
chimeric gene containing this promoter and transgenic plant.
ACCESSION BD128389
VERSION BD128389.1 GI:23223334
KEYWORDS JP 2002500016-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1021)
AUTHORS Durose,R. and Freysinet,G.
TITLE Corn H3c4 promoter bonded to the first intron of rice actin,
chimeric gene containing this promoter and transgenic plant
JOURNAL Patent: JP 2002500016-A 1 08-JAN-2002;
COMMENT AVENTIS CROPS SCIENCE SA
OS Unidentified
PN JP 2002500016-A/1
PD 08-JAN-2002
PF 22-DEC-1998 JP 2000526660
PR 24-DEC-1997 FR 97/16726
PI RICHARD DUROSE, GEORGES FREYSINET
PC C12N15/09,A01H5/00,C07K14/21,C07K14/415,C07K19/00,C12N5/10, PC
C12Q1/68,
PC C12N15/00,C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
CC Corn H3c4 promoter bonded to the first intron of rice actin,
chimeric gene
CC containing this promoter and transgenic plant FH Key
CC Location/Qualifiers
FT 1..1021
FT source /organism='unidentified'.
LOCATION/QUALIFIERS
1..1021
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
ORIGIN
Query Match 65.2%; Score 1021; DB 6; Length 1021;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 CTTATGCGACCATTTACTGTATGATGATATCATATTTAATGAAGCAAACTTTCTATT 86
DB 1 CTTATGCGACCATTTACTGTATGATGATATCATATTTAATGAAGCAAACTTTCTATT 60
QY 87 ACTTCTTTACTAATCATATTTCTGTGTTTAAATTCAGTCTCAACATTCATTGCTCAAG 146
DB 61 ACTTCTTTACTAATCATATTTCTGTGTTTAAATTCAGTCTCAACATTCATTGCTCAAG 120
QY 147 TATTAAGTTGAGCTGTCAAAATTTACTATTTTATTTCTTCATATTTTCTTCTATACA 206
DB 121 TATTAAGTTGAGCTGTCAAAATTTACTATTTTATTTCTTCATATTTTCTTCTATACA 180
QY 207 GATTTGGGCTTACATCATCATATATCATATTCATTCCTGCGTCCCTTAAAGATT 266
DB 181 GATTTGGGCTTACATCATCATATATCATATTCATTCCTGCGTCCCTTAAAGATT 240
QY 267 CCATCTCTGAAATCTTATCTCTCCAAATAGCTTCTTAATCAGGTCCTTAAGCAA 326
DB 241 CCATCTCTGAAATCTTATCTCTCCAAATAGCTTCTTAATCAGGTCCTTAAGCAA 300
QY 327 TACCTATATTAGAGACATTTTATTTTGTATACATATTTGTCATATCTCAAGT 386
DB 301 TACCTATATTAGAGACATTTTATTTTGTATACATATTTGTCATATCTCAAGT 360
QY 387 CATTAATCATATTTAGTTTACTTAAACGATTTATTTAAAGTAAAGGATGAAAGAAC 446
DB 361 CATTAATCATATTTAGTTTACTTAAACGATTTATTTAAAGTAAAGGATGAAAGAAC 420
QY 447 TGTTAGATTAATTTCTATATATAGAGATCCAGTAGCGTCTCTAAATTTAGATGATTAT 506

DB 421 TGTTAGATTAATTTCTATATATAGAGATCCAGTAGCGTCTCTAAATTTAGATGATTAT 480
QY 507 TTAGAGAGCGCGTTAGAAAACGTAAAAATTTCTTGAATTTATTTATTTAGGGTAGAGT 566
DB 481 TTAGAGAGCGCGTTAGAAAACGTAAAAATTTCTTGAATTTATTTATTTAGGGTAGAGT 540
QY 567 AGCCTTTATGCTTTATAGATCTTTGTTGAGACCCAGCCTTAATACCGTTATTTTCGCATT 626
DB 541 AGCCTTTATGCTTTATAGATCTTTGTTGAGACCCAGCCTTAATACCGTTATTTTCGCATT 600
QY 627 GCGCTCTCATTTTCACTTCACGCGCCCAATTTTCAAGTTTCAACGAGCGCCAGCC 686
DB 601 GCGCTCTCATTTTCACTTCACGCGCCCAATTTTCAAGTTTCAACGAGCGCCAGCC 660
QY 687 TGCCATACCAAAATTTGGTACGGTGGGCGGTTTCAAAAAGAGTCGGAACCATCTGC 746
DB 661 TGCCATACCAAAATTTGGTACGGTGGGCGGTTTCAAAAAGAGTCGGAACCATCTGC 720
QY 747 ACCCAACCGACTAGTAGGCGCTCGATTCCTCCCTGATTAAGTCTTAAGCCAAATAGAGCCCA 806
DB 721 ACCCAACCGACTAGTAGGCGCTCGATTCCTCCCTGATTAAGTCTTAAGCCAAATAGAGCCCA 780
QY 807 GAACCAACCATACCGCGATCGTCCCTACGCTTCACTCATCGCGCGCTCATCTCCA 866
DB 781 GAACCAACCATACCGCGATCGTCCCTACGCTTCACTCATCGCGCGCTCATCTCCA 840
QY 867 TCCAAACCATATTCGTTACCTTACCTTGCCTCCGAAATTTCTCGGCTCGGCTCCGC 926
DB 841 TCCAAACCATATTCGTTACCTTACCTTGCCTCCGAAATTTCTCGGCTCGGCTCCGC 900
QY 927 ACTTACTCAAAATACCAATCCCATCCATCAGACGATGCACTATGCAAAATCCCGAGAA 986
DB 901 ACTTACTCAAAATACCAATCCCATCCATCAGACGATGCACTATGCAAAATCCCGAGAA 960
QY 987 ATCAACACTCCCAATTTCCAGCTGCGACCAACTGCGGCTCTCCGCGCAACGACCAA 1046
DB 961 ATCAACACTCCCAATTTCCAGCTGCGACCAACTGCGGCTCTCCGCGCAACGACCAA 1020
QY 1047 G 1047
DB 1021 G 1021
RESULT 7
A94724 454 bp DNA linear PAT 26-JUN-2000
LOCUS A94724
DEFINITION Sequence 2 from Patent WO934005.
ACCESSION A94724
VERSION A94724.1 GI:678989
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 454)
AUTHORS Durose,R. and Freysinet,G.
TITLE MAIZE H3c4 PROMOTER ASSOCIATED WITH FIRST RICE ACTIN INTRON,
CHIMERIC GENE CONTAINING IT AND TRANSFORMED PLANT
JOURNAL Patent: WO 934005-A 2 08-JUL-1993;
Rhone Poulenc Agrochimie (FR)
FEATURES
source 1..454
/organism='unidentified'
/mol_type='unassigned DNA'
/db_xref='taxon:32644'
ORIGIN
intron
Query Match 29.0%; Score 454; DB 6; Length 454;
Best Local Similarity 100.0%; Pred. No. 2e-238;
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1102 GTAACCAACCCGCCCT 1161

Dd	1	GTAAACACCCGCCCCCTCTCCCTCTTCTCTTCGCTTCTCGCTTTTCTTCTCGAT	60
Oy	1162	CTTTGGCCTTGAGTTGGGTGGGCGAGAGCGCTTGTGCGCCAGATCGGTGGCGGG	1221
Dd	61	CTTTGGCCTTGAGTTGGGTGGGCGAGAGCGCTTGTGCGCCAGATCGGTGGCGGG	120
Oy	1222	AGGGCGGGGAGTCTCGCGGCTGGCGCTCCCGGGCGGAGTCCGCGCCGAGTCTCCCGGGGA	1281
Dd	121	AGGGCGGGGAGTCTCGCGGCTGGCGCTCCCGGGCGGAGTCCGCGCCGAGTCTCCCGGGGA	180
Oy	1282	ATGGGGCTCTCGAGATGATCTGATTCGCGCGTGTGTGGGGAGATGATGGGGGTTAA	1341
Dd	181	ATGGGGCTCTCGAGATGATCTGATTCGCGCGTGTGTGGGGAGATGATGGGGGTTAA	240
Oy	1342	AATTTGCGCATGCTAAACAAGATCAGAAAGGGGAAAAAGGCACTATGTTTATATTT	1401
Dd	241	AATTTGCGCATGCTAAACAAGATCAGAAAGGGGAAAAAGGCACTATGTTTATATTT	300
Oy	1402	TATATATTTTCTGCTGCTGCTGTCAGGCTTGATGTGCTAATCTTTTCTTCTTTT	1461
Dd	301	TATATATTTTCTGCTGCTGCTGTCAGGCTTGATGTGCTAATCTTTTCTTCTTTT	360
Oy	1462	GTGGGTAAATTTGAATCCCTCAGATGTCATGGTAGTTTTCTTTCAATATTTG	1521
Dd	361	GTGGGTAAATTTGAATCCCTCAGATGTCATGGTAGTTTTCTTTCAATATTTG	420
Oy	1522	GACAAATCAGCCTGTGCGAGAGCTTTTGTAG	1555
Dd	421	GACAAATCAGCCTGTGCGAGAGCTTTTGTAG	454

LOCUS	AR559744	454 bp	DNA	linear	PAT 08-OCT-2004
DEFINITION	Sequence 2 from patent US 6750378.				
ACCESSION	AR559744				
VERSION	AR559744.1	GI:53969842			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 454)				
TITLE	Derose,R., and Freyssainet,G. Maize H3C4 promoter combined with the first intron of rice actin, chimeric gene comprising it and transformed plant Patent: 6750378-A 2 15-JUN-2004;				
JOURNAL	Location/Qualifiers				
FEATURES	1..454				
source	/organism="unknown" /mol_type="genomic DNA"				
ORIGIN					
Query Match	29.0%; Score 454; DB 6; Length 454;				
Best Local Similarity	100.0%; Pred. No. 2e-238;				
Matches 454; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
QY	1102	GTAACCACCCCGCCCCCTCTCCTCTTCTCTTTCTTCGCTTTTTTTTTTGCTCGGTCTGCAT	1161		
DB	1	GTAACCAACCCGCCCCCTCTCCTCTTCTTCTTCGCTTTTTTTTTTGCTCGGTCTGCAT	60		
QY	1162	CTTTGGCCTTGAGTAGTTGGGCTGGGCGAGAGCGGCTTGTGTGCCAGATCGGTGGCGGG	1221		
DB	61	CTTTGGCCTTGAGTAGTTGGGCTGGGCGAGAGCGGCTTGTGTGCCAGATCGGTGGCGGG	120		
QY	1222	AGGGGCGGGATCTCGCGGCTGGCGCTCTCCGGGCGTGAATCGGCCCGGATCCTTCGCGGGGA	1281		
DB	121	AGGGGCGGGATCTCGCGGCTGGCGCTCTCCGGGCGTGAATCGGCCCGGATCCTTCGCGGGGA	180		
QY	1282	ATTGGGACTCTCGGAGTGTGATGTGATTCGCGCGCTTGTGGGGGAGATGATGGGAGCTTTAA	1341		
DB	181	ATTGGGACTCTCGGAGTGTGATGTGATTCGCGCGCTTGTGGGGGAGATGATGGGAGCTTTAA	240		

Accession	Sequence	Length
QY	1342 AATTTCGCATGCTAAACAAATCAGAGAGGGGAAAAGGGCACTATGTTTATATTT	1401
Db	241 AATTTCGCATGCTAAACAAATCAGAGAGGGGAAAAGGGCACTATGTTTATATTT	300
QY	1402 TATATATTCTGCTGCTGCTGCTCAGGCTTAGATGCTAGATCTTTCTCTCTTTT	1461
Db	301 TATATATTCTGCTGCTGCTGCTCAGGCTTAGATGCTAGATCTTTCTCTCTTTT	360
QY	1462 GTGGGTGAATTGAATCCCTCAGCATTTGTCATCGGAGTTTCTTTTCATGATTTGT	1521
Db	361 GTGGGTGAATTGAATCCCTCAGCATTTGTCATCGGAGTTTCTTTTCATGATTTGT	420
QY	1522 GACAAATGCAGCTCTGTGCGAGGCTTTTGTAG 1555	
Db	421 GACAAATGCAGCTCTGTGCGAGGCTTTTGTAG 454	

[illegible]

QY	1282	ATGGGGGCTCTGGAGATGATCTGATTCGGCGTGTGTGGGGGAGATGATGAGGGCGTTAA	1341
Db	181	ATGGGGCTCTGGAGATGATCTGATTCGGCGTGTGTGGGGGAGATGATGAGGGCGTTAA	240
QY	1342	AATTTTGGCATGCTTAAACAAGATCAGAAAGGGGAAAAGGCACTATGTTTATATTTT	1401
Db	241	AATTTTGGCATGCTTAAACAAGATCAGAAAGGGGAAAAGGCACTATGTTTATATTTT	300
QY	1402	TATATATTCTGCTGCTGCTGCTGAGGCTTGATGTGCTAGATCTTTCTTTCTTTT	1461
Db	301	TATATATTCTGCTGCTGCTGCTGAGGCTTGATGTGCTAGATCTTTCTTTCTTTT	360
QY	1462	GTGGGTAGATTTGATCCCTCAGCATTTTCATCGTAGTTTTCCTTTCAATATTTGT	1521
Db	361	GTGGGTAGATTTGATCCCTCAGCATTTTCATCGTAGTTTTCCTTTCAATATTTGT	420
QY	1522	GACCAATGCAGCTCTGTGGGAGCTTTTGTGAG	1555
Db	421	GACCAATGCAGCTCTGTGGGAGCTTTTGTGAG	454

RESULT	10				
LOCUS	MZEH3C4	1264 bp	DNA	linear	PLN 27-APR-1993
DEFINITION	Maize (Zea mays) histone H3 gene (H3C4), complete cds.				
ACCESSION	M13379				
VERSION	M13379.1	GI:168496			
KEYWORDS	histone				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 1264)				
TITLE	Chabert,N., Phillips,G., Chaboute,M.-E., Enling,M. and Gigot,C. Nucleotide sequences of two corn histone H3 genes				
JOURNAL	organization of the corn histone H3 and H4 genes				
COMMENT	Plant Mol. Biol. 6, 253-263 (1986)				
FEATURES	Original source text: Maize DNA, clone H3C4.				
SOURCE	Drift entry and printed copy of the sequence [1] kindly provided by C.Gigot, 10-OCT-1986.				
location/Qualifiers					
1..1264					
/organism="Zea mays"					
/mol_type="genomic DNA"					
/db_xref="taxon:4577"					
526..936					
/note="histone H3"					
/codon_start=1					
/protein_id="AA13473.1"					
/db_xref="GI:168497"					
/translation="MARTKQTPARKSTGSKAPRKQLATTAARKAPATGCVKKPHRFRE GTVLAIREIKYQKSTELIRKLPQRLVRELAQPKTLRFOSSVAALQBAAEAYIVL GLFEDTNLCALHAKRVITMPKDIOQLARRIRGERA"					
ORIGIN	54 bp upstream of BglII site.				
Query Match	25.6%;	Score 400;	DB 8;	Length 1264;	
Best Local Similarity	100.0%;	Pred. No. 1.4e-208;			
Matches 400;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
648	GGCCCCACATTTTCACGTTTTCACCGAAGCGCCAGCTGCGCTAACCAACAATTGGTA	707			
120	GGGCCCACTTTTACCGTTTTCACCGAAGCGCCAGCTGCGCTAACCAACAATTGGTA	179			
708	CGGTGGCGGTTTCAAAAGAAGTCGGAACCATCTGACCCACCGACTAGTAGGCGCT	767			
180	CGGTGGCGGTTTCAAAAGAAGTCGGAACCATCTGACCCACCGACTAGTAGGCGCT	239			
768	CGGATCCCTCCGATTAGTGCTTACGCAATAGAGCCCAAGACCAACCATACGGCGATC	827			
240	CGGATCCCTCCGATTAGTGCTTACGCAATAGAGCCCAAGACCAACCATACGGCGATC	299			

QY 828 TTCCCTAGCGTTCCACCGCATCGGGGGCGGTGCATCTCATCTCAACACCTATTCCGTTAC 887

Db 300 GTCCCTAGCGTTCCACCGCATCGGGGGCGGTGCATCTCATCTCAACACCTATTCCGTTAC 359

QY 888 TTGCCCATCTCCGAAAAAATTCTCGGCTCGGCTCGGACCTATCTACAAATACCATCC 947

Db 360 TTGCCCATCTCCGAAAAAATTCTCGGCTCGGCTCGGACCTATCTACAAATACCATCC 419

QY 948 CATCAGCAGCATGGCATCACTGGCAAAATCCCCCGAAAAATCAACACTCTCCCAATTCCAC 1007

Db 420 CATCAGCAGCATGGCATCACTGGCAAAATCCCCCGAAAAATCAACACTCTCCCAATTCCAC 479

QY 1008 GGTGCGAACCACTGGCGGTCTCTCGCGCGCAAGCAACAAG 1047

Db 480 GGTGCGAACCACTGGCGGTCTCTCGCGCGCAAGCAACAAG 519

RESULT 11	LOCUS	AX467609	623 bp	DNA	linear	PAT 16-JUL-2002
	DEFINITION	Sequence 19 from Patent WO0234926.				
	ACCESSION	AX467609				
	VERSION	AX467609.1	GI:21900797			
	KEYWORDS					
	SOURCE					
	ORGANISM	Oryza sativa				
		Oryza sativa				
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
		Ehrhartoideae; Oryzaceae; Oryza.				
	REFERENCE					
	AUTHORS	Sticklen,M.B., Dale,B.E. and Magpool,S.				
	TITLE	Transgenic plants containing ligninase and cellulase which degrade				
		lignin and cellulose to fermentable sugars				
		Patent: WO 0234926-A 19 02-MAY-2002;				
	JOURNAL	MICHIGAN STATE UNIVERSITY (US)				
	FEATRES					
	source	location/Qualifiers				
		1..623				
		/organism="Oryza sativa"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:4530"				
	ORIGIN					
	Query Match	18.9%; Score 296; DB 6; Length 623;				
	Best Local Similarity	100.0%; Pred.No.3.6e-151;				
	Matches 296; Conservative	0; Mismatches 0; Indels 0; Gaps 0				
QY	1265	CCGATCTCTCCGCGGGGAATGTGGGGCTCTCGATGTGATCTGTATCCGCCGTTGTTGGGGGA	1324			
DB	278	CCGATCTCTCCGCGGGGATGGGGCTCTCGATGTGATCTGTATCCGCCGTTGTTGGGGGA	337			
QY	1335	GATGATGGGGCGTTAAAAATTTCCGCATGCTPAACAAGATCAAGAAAGGGGAAAAAGGC	1384			
DB	338	GATGATGGGGCGTTAAAAATTTCCGCATGCTPAACAAGATCAAGAAAGGGGAAAAAGGC	397			
QY	1385	ACTATGATTTATTTATATATATTTCTGCTGCTGCTGTCAGGCTTGATGTGCTAGAT	1444			
DB	398	ACTATGATTTATTTATATATATTTCTGCTGCTGCTGTCAGGCTTGATGTGCTAGAT	457			
QY	1445	CTTTCCTTCTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTGTTTCATCGTAGATT	1504			
DB	458	CTTTCCTTCTTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTGTTTCATCGTAGATT	517			
QY	1505	TTCTTTTCATGATTTGTGACAAATGACACCTCGTGGGAGCTTTTGTAGGTAGA	1560			
DB	518	TTCTTTTCATGATTTGTGACAAATGACACCTCGTGGGAGCTTTTGTAGGTAGA	573			
RESULT 12						
	LOCUS	OSACT1	623 bp	DNA	linear	PLN 24-MAR-1999
	DEFINITION	O.sativa Act1 gene.				
	ACCESSION	X63830				
	VERSION	X63830.1	GI:468505			

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 03:55:48 ; Search time 896.833 Seconds
(without alignments)
10330.128 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565
Sequence: 1 GAATTCCTGACGAGTCGACG.....TTTTTTGTAGTACGACCAG 1565

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1565	100.0	1565	2	AAZ91039
2	1021	65.2	1021	2	AAZ91037
3	454	29.0	454	2	AAZ91038
4	296	18.9	623	3	AAZ47117
5	296	18.9	623	6	ABK86738
6	296	18.9	1392	2	AAT80053
7	296	18.9	2199	2	AAT80052
8	296	18.9	5643	2	AAT80055
9	294	18.8	470	6	ABT07357
10	294	18.8	470	10	ADF49181
11	236	15.1	1259	6	ADG69912
12	236	15.1	1259	11	ADN88926
13	236	15.1	3657	6	ADG69892
14	236	15.1	4604	6	ADG69905
15	236	15.1	4773	6	ADG69901
16	236	15.1	4773	11	ADN88915
17	236	15.1	4950	6	ADG69903
18	236	15.1	4950	11	ADN88917
19	236	15.1	4965	6	ADG69906
20	236	15.1	4974	6	ADG69904

21	236	15.1	4974	11	ADN88918	Adn88918 pU04 vect
22	236	15.1	5164	11	ADN88919	Adn88919 pP010.1 v
23	236	15.1	5267	11	ADN88907	Adn88907 pTP8-5 ve
24	236	15.1	5277	6	ADG69894	Adg69894 Vector pT
25	236	15.1	5277	11	ADN88909	Adn88909 pTP5-1 ve
26	236	15.1	5295	6	ADG69907	Adg69907 Vector pU
27	236	15.1	5295	11	ADN88922	Adn88922 pU04 vect
28	236	15.1	5327	6	ADG69896	Adg69896 Vector pT
29	236	15.1	5327	11	ADN88911	Adn88911 pTP42 ve
30	236	15.1	5337	6	ADG69888	Adg69888 Vector pU
31	236	15.1	5337	6	ADG69900	Adg69900 Vector pT
32	236	15.1	5337	11	ADN88914	Adn88914 pTP5 vect
33	236	15.1	5337	11	ADN88903	Adn88903 pTP4 vect
34	236	15.1	5338	6	ADG69884	Adg69884 Vector pT
35	236	15.1	5338	6	ADG69898	Adg69898 Vector pT
36	236	15.1	5338	11	ADN88913	Adn88913 pTP3-1 ve
37	236	15.1	5338	11	ADN88899	Adn88899 pTP10-1 v
38	236	15.1	5345	6	ADG69886	Adg69886 Vector pU
39	236	15.1	5345	11	ADN88901	Adn88901 pU04-4 ve
40	236	15.1	5387	6	ADG69910	Adg69910 Vector pT
41	236	15.1	5387	11	ADN88925	Adn88925 pTP11-1 v
42	236	15.1	5395	6	ADG69890	Adg69890 Vector pT
43	236	15.1	5395	11	ADN88905	Adn88905 pTP5.14 v
44	236	15.1	5510	2	AA012707	Aag12707 Rice acti
45	236	15.1	5595	11	ADN88920	Adn88920 pU03 vect

ALIGNMENTS

RESULT 1	
AAZ91039	AAZ91039 standard; DNA; 1565 BP.
ID	
XX	
AC	AAZ91039;
XX	
DT	17-OCT-2003 (revised)
DT	06-JUN-2000 (first entry)
XX	
DE	Chimeric maize H3C4 promoter/rice actin gene intron 1 regulatory region.
XX	
KW	Regulatory element; monocotyledonous vegetable plant cell; maize;
KW	histone H3C4; promoter; rice actin gene intron; chimeric; ss;
XX	herbicide resistance.
OS	Zea mays.
OS	Oryza sativa.
OS	Chimeric.
PN	FR2772787-A1.
XX	
PD	25-JUN-1999.
XX	
PF	24-DEC-1997; 97FR-00016726.
XX	
PR	24-DEC-1997; 97FR-00016726.
XX	
PA	(RHON) RHONE-POULENC AGROCHIMIE.
XX	
PI	Derose R, Freysinet G;
XX	
DR	WPI; 1999-397352/34.
PT	5' chimeric regulatory region comprising maize histone H3C4 promoter and
PT	rice actin gene first intron.
XX	
PS	Claim 8; Page 15-16; 24pp; French.
XX	
CC	The invention relates to a DNA sequence comprising a 5' regulatory
CC	element for the expression of a heterologous gene in a monocotyledonous
CC	vegetable plant cell. The DNA (this sequence) comprises: (a) a functional
CC	fragment of the maize histone H3C4 promoter sequence (AAZ91037; and (b) a
CC	functional fragment of the first intron of the rice actin gene

(AAZ91038). The chimeric regulatory region is useful for the expression of heterologous genes that confer resistance to certain herbicides, or that have novel agronomical properties in monocotyledons. In particular, the chimeric 5' regulatory gene is linked to an enzyme that confers resistance to a specific herbicide. This is useful for controlling weeds in fields of plants/grains that have been transformed with the chimeric gene. The herbicide can be applied to the field without affecting the plant/grain. (Updated on 17-Oct-2003 to standardise OS field)

XX Sequence 1565 BP; 366 A; 415 C; 297 G; 487 T; 0 U; 0 Other;

Query Match 100.0%; Score 1565; DB 2; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GAATTCCTGACGATGACGATCCCTTATGACACATTTCTGTAATGCAATCAT 60
DB 1 GAATTCCTGACGATGACGATCCCTTATGACACATTTCTGTAATGCAATCAT 60
QY 61 TTAATTGAATAGCAAACTTTCTATTACTCTTACTAACAATATCTGGTTTAAAT 120
DB 61 TTAATTGAATAGCAAACTTTCTATTACTCTTACTAACAATATCTGGTTTAAAT 120
QY 121 TCAAGTCTCAACATTCATGCTCAAGTATAGTTGAGACTGTCAAAATTTACTATTAT 180
DB 121 TCAAGTCTCAACATTCATGCTCAAGTATAGTTGAGACTGTCAAAATTTACTATTAT 180
QY 181 TTCTTCAATATTTTTTCTCTTATACACATTTTGGGCTTACATCATCATATATCA 240
DB 181 TTCTTCAATATTTTTTCTCTTATACACATTTTGGGCTTACATCATCATATATCA 240
QY 241 TCCCTTCCGGTGTCTCTAATAAGATTCATCTCTGATCTTATTCCTCCATACAGT 300
DB 241 TCCCTTCCGGTGTCTCTAATAAGATTCATCTCTGATCTTATTCCTCCATACAGT 300
QY 301 TCTCTAATATCAGGTCTCTATAGCAATACCTATATTAGAGACATTTTATTTTTGTAC 360
DB 301 TCTCTAATATCAGGTCTCTATAGCAATACCTATATTAGAGACATTTTATTTTTGTAC 360
QY 361 ATACATATTTGTATCTCAATGATATATATATTTAGTTTACTTAAACCATATAT 420
DB 361 ATACATATTTGTATCTCAATGATATATATATTTAGTTTACTTAAACCATATAT 420
QY 421 TTAAGATATCAACGATGAGAACTGTTAGATAAATCTATATATAGAAATCAAGT 480
DB 421 TTAAGATATCAACGATGAGAACTGTTAGATAAATCTATATATAGAAATCAAGT 480
QY 481 AGCGTTCCTAATAATTTAGATGATTTATAGAGACGCTGTAGAAAAAGTAAATTTCT 540
DB 481 AGCGTTCCTAATAATTTAGATGATTTATAGAGACGCTGTAGAAAAAGTAAATTTCT 540
QY 541 TTGATTTATTTATTTTAGGATAGATAGCTTTATATGTTTATGATCTTTGGTGACCA 600
DB 541 TTGATTTATTTATTTTAGGATAGATAGCTTTATATGTTTATGATCTTTGGTGACCA 600
QY 601 GCGTTATACCGGTTATTTTGGCAATGCGCTCTCATTTTCACTCCAGGCCCCACATTT 660
DB 601 GCGTTATACCGGTTATTTTGGCAATGCGCTCTCATTTTCACTCCAGGCCCCACATTT 660
QY 661 TCAAGTTTTTCAACGAGCGCCAGCTGCTTAAACCAAAATTTGTAGCGGTGGCGGTT 720
DB 661 TCAAGTTTTTCAACGAGCGCCAGCTGCTTAAACCAAAATTTGTAGCGGTGGCGGTT 720
QY 721 TTCAAAAGAAATGGGAAACATCTGCAACCGACATGATAGGCGCTCGGATCTCTCTG 780
DB 721 TTCAAAAGAAATGGGAAACATCTGCAACCGACATGATAGGCGCTCGGATCTCTCTG 780
QY 781 ATTAAGCTTAGGCAATAGAGGCCAGAACCCATCAAGCGGATGTGCTTACGCTTC 840
DB 781 ATTAAGCTTAGGCAATAGAGGCCAGAACCCATCAAGCGGATGTGCTTACGCTTC 840
QY 841 CACCTGATCGGCGCGGTCAATCTCAACCAACTATTCGTTACCTTGGCCATCTCC 900
DB 841 CACCTGATCGGCGCGGTCAATCTCAACCAACTATTCGTTACCTTGGCCATCTCC 900

```

```

DB 841 CACCTGATCGGCGCGGTCAATCTCAACCAACTATTCGTTACCTTGGCCATCTCC 900
QY 901 GAAAAAATTTCTGAGCTCGAGCTCCGACCTACTAACAATACCATCCATCCATCAGACGAT 960
DB 901 GAAAAAATTTCTGAGCTCGAGCTCCGACCTACTAACAATACCATCCATCCATCAGACGAT 960
QY 961 CGCATCACTGCCAAATCCCGCAAAAATCAACACTCTCCAAATTCAGCGCTGCACCAACT 1020
DB 961 CGCATCACTGCCAAATCCCGCAAAAATCAACACTCTCCAAATTCAGCGCTGCACCAACT 1020
QY 1021 CGCGTCTCTCCGCGCAAGACCAAAAGAAATTTGGCGGACACCGCGTGAAGTCTCTCC 1080
DB 1021 CGCGTCTCTCCGCGCAAGACCAAAAGAAATTTGGCGGACACCGCGTGAAGTCTCTCC 1080
QY 1081 CCGCCCGCTCCGCGCGCGCGGATACCAACCGCCCTCTCTCTTTCTTTCTCGGTTT 1140
DB 1081 CCGCCCGCTCCGCGCGCGCGGATACCAACCGCCCTCTCTCTTTCTTTCTCGGTTT 1140
QY 1141 TTTTTCGTCTGATCTCGATCTTTTGGCTTTGAGTTTGGTGGGCGAGAGCGGCTTCG 1200
DB 1141 TTTTTCGTCTGATCTCGATCTTTTGGCTTTGAGTTTGGTGGGCGAGAGCGGCTTCG 1200
QY 1201 TCGCCCAATCGGTGCGCGGAGGCGGAGATCTCGCGCTGGCGCTCCGCGCGTGAAT 1260
DB 1201 TCGCCCAATCGGTGCGCGGAGGCGGAGATCTCGCGCTGGCGCTCCGCGCGTGAAT 1260
QY 1261 CGGCGCGGATCTCTCGCGGGAATGGGAGCTCTCGATGATAGTCTGATCGCGCTGTGG 1320
DB 1261 CGGCGCGGATCTCTCGCGGGAATGGGAGCTCTCGATGATAGTCTGATCGCGCTGTGG 1320
QY 1321 GGGAGATGATGGGAGGCTTTAAATTTGCGCATGTAAACAAGATCAGAAAGGAGAAA 1380
DB 1321 GGGAGATGATGGGAGGCTTTAAATTTGCGCATGTAAACAAGATCAGAAAGGAGAAA 1380
QY 1381 GGGACATATGTTTATTTTATATTTTCTGCTGCTGCTGCTGACAGCTTATGATGCT 1440
DB 1381 GGGACATATGTTTATTTTATATTTTCTGCTGCTGCTGCTGACAGCTTATGATGCT 1440
QY 1441 AGATCTTCTCTCTTTTGTGGTGAATTTGAATCCCTCAGCATTTGTCATCGGTA 1500
DB 1441 AGATCTTCTCTCTTTTGTGGTGAATTTGAATCCCTCAGCATTTGTCATCGGTA 1500
QY 1501 GTTTTCTTTTATGATTTTGAACAATGACGCTGTGCGGAGCTTTTGTAGGTAGA 1560
DB 1501 GTTTTCTTTTATGATTTTGAACAATGACGCTGTGCGGAGCTTTTGTAGGTAGA 1560
QY 1561 CCATG 1565
DB 1561 CCATG 1565

RESULT 2
AAZ91037
ID AAZ91037 standard; DNA; 1021 BP.
XX
XX AAZ91037;
XX
XX 06-JUN-2000 (first entry)
XX
XX Maize histone H3C4 promoter region.
XX
XX Regulatory element; monocotyledonous vegetable plant cell; maize;
XX histone H3C4; promoter; rice actin gene intron; chimeric; ss;
XX herbicide resistance.
XX
XX Zea mays.
XX
XX FR2772787-A1.
XX
XX 25-JUN-1999.
XX
XX 24-DEC-1997; 97PR-00016726.
XX

```


Db 518 TTCTTTTCATGATTGTGACAAATGACAGCTCGTGGGAGCTTTTGTAGTAGA 573

RESULT 5
ABK86738
ID ABK86738 standard; DNA; 623 BP.
XX
XX ABK86738;
XX
XX 24-SEP-2002 (first entry)
XX
XX
XX Rice Act1 gene.
DE
XX
XX Rice; gene; ds; transgenic; plant; lignocellulose; cellulase; ligninase;
KM fermentable sugar; ethanol; fermentation; silage; feed; fuel;
KM industrial chemical; biodegradation; chloroaromatic;
XX environmental pollutant; Act1.
XX
XX Oryza sativa.
OS
XX
XX WO200234926-A2.
PN
XX
XX 02-MAY-2002.
PD
XX
XX 18-OCT-2001; 2001WO-US032538.
PF
XX
XX 20-OCT-2000; 2000US-0242408P.
PR
XX
XX (UNMS) UNIV MICHIGAN STATE.
PA
XX
XX Sticklen MB, Dale BE, Magdool S;
PI
XX
XX WPI; 2002-489947/52.
DR
XX
XX
XX Producing transgenic plants which after harvest degrade lignin and
PT cellulose to fermentable sugars, by mating transgenic plant comprising
PT DNA encoding cellulase with transgenic plant comprising DNA encoding
PT ligninase.
XX
XX
XX Example 1; Page 124; 126pp; English.
PS
XX
XX The invention discloses the production of a transgenic plant which
CC degrades lignocellulose when the plant is ground. It comprises the
CC production of the transgenic plant including cellulase and ligninase by
CC mating a transgenic plant, containing a DNA encoding a cellulase, and a
CC transgenic plant, containing a DNA encoding a ligninase, where both genes
CC are operably linked to a nucleotide sequence encoding a signal peptide
CC which targets the fusion protein to an organelle of the plant,
CC particularly chloroplasts. The method is useful for producing a
CC transgenic plant (e.g. maize) which degrades lignocellulose when the
CC plant is ground to produce a plant material. This material is useful for
CC converting lignocellulose, in a plant material, to fermentable sugars
CC which are then fermented to ethanol. The transgenic plants also provide a
CC plentiful and inexpensive source of fungal or bacterial cellulases and
CC ligninases which can be used in the production of ethanol. They can also
CC be used for pre-treating silage to increase the energy value of
CC lignocellulosic feeds for cows and other ruminant animals, pre-treating
CC lignocellulosic biomass for fermentative conversion to fuels and
CC industrial chemicals, and biodegradation of chloroaromatic environmental
CC pollutants. The sequence presented is the rice Act1 gene and promoter
XX
XX
SQ Sequence 623 BP; 98 A; 184 C; 164 G; 177 T; 0 U; 0 Other;
Query Match 18.9%; Score 296; DB 6; Length 623;
Best Local Similarity 100.0%; Pred. No. 6,2e-130;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1265 CCGATCTCTCGCGGGGAATGGGCGCTCTCGATGTAGATTCGCGCGTTGTTGGGGGA 1324
278 CCGATCTCTCGCGGGGAATGGGCGCTCTCGATGTAGATTCGCGCGTTGTTGGGGGA 337
1325 GATATGGGGCGTTTAAATTTCCCATGCTAAACAAGATAGAAAGGGAAGAGGC 1384

Db 338 GATGATGGGGCGTTTAAATTTGCCATGCTAAACAAGATCAGAAAGGGAAGAGGC 397

QY 1385 ACTATGTTTATATTTTATATATTTTCTGCTGCTGCTCAGGCTTAATGTGCTAGAT 1444
DB 398 ACTATGTTTATATTTTATATATTTTCTGCTGCTGCTCAGGCTTAATGTGCTAGAT 457

QY 1445 CTTTCCTTCTCTCTTTTGGGGGAGAAATTGAAATCCCTGAGCATTTGTCAGGTTAGTT 1504
DB 458 CTTTCCTTCTCTCTTTTGGGGGAGAAATTGAAATCCCTGAGCATTTTCAATGCTAGTT 517

QY 1505 TTCTTTTCATGATTGTGACAAATGACAGCTCGTGGGAGCTTTTGTAGTAGA 1560
Db 518 TTCTTTTCATGATTGTGACAAATGACAGCTCGTGGGAGCTTTTGTAGTAGA 573

RESULT 6
AAT80053
ID AAT80053 standard; cDNA; 1392 BP.
XX
XX
XX AAT80053;
AC
XX
XX 25-MAR-2003 (revised)
DT
DT 04-NOV-1997 (first entry)
XX
XX
XX Rice actin 1 gene promoter fragment.
DE
XX
XX Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;
KM cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.
XX
XX
XX Oryza sativa.
OS
XX
XX US5641876-A.
PN
XX
XX 24-JUN-1997.
PD
XX
XX 27-OCT-1993; 93US-00144602.
PF
XX
XX 05-JAN-1990; 90US-00461490.
PR
PR 18-SEP-1991; 91US-00762680.
XX
XX
XX (CORR) CORNELL RES FOUND INC.
PA
XX
XX Wu R, McElroy D;
PI
XX
XX WPI; 1997-340996/31.
DR
XX
XX
XX Nucleic acid containing the promoter of the rice actin-1 gene - used to
PT direct efficient expression of foreign genes in rice.
PT
XX
XX Claim 4; Col 35-38; 29pp; English.
PS
XX
XX This sequence represents a fragment from the promoter region of the rice
CC actin-1 (Rac1) gene. Cytoplasmic actin is a fundamental and essential
CC component of the eukaryotic cell and cytoskeleton. In higher plant cells,
CC a number of cellular processes, such as cytoplasmic streaming, extension
CC growth and cell division are thought to involve the cytoskeletal actin
CC protein. All of the studied plant actins consist of four exons of
CC conserved length, separated by 3 introns of variable length. In rice
CC there are at least 8 actin-like sequences per haploid genome. Rac1
CC encodes a transcript that is relatively abundant in all rice tissues.
CC This sequence is an example of a nucleic acid molecule of the invention.
CC The nucleic acid molecules of the invention contain the Rac1 gene (or
CC fragments) with promoter activity in monocotyledonous plants. The
CC promoter is used to direct expression of foreign genes in transgenic rice
CC and other plants. The actin promoter is more efficient in rice
CC transformation than previously proposed promoters (e.g. 5 times more
CC active than the maize Adh1 promoter) and has constitutive activity in
CC space and time. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX
SQ Sequence 1392 BP; 376 A; 343 C; 309 G; 364 T; 0 U; 0 Other;
Query Match 18.9%; Score 296; DB 2; Length 1392;
Best Local Similarity 100.0%; Pred. No. 6.1e-130;

	Matches	296;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1265	CCGAGTCTTCGCGGGGAAGTGGGCTCTTCGATGTAGATCTGATCCGCGTTGTTGGGGA								1324
Db	1076	CCGGATCCTCGCGGGGAATGGGGCTCTCGAGTGTAGATCTGATCCGCGTTGTTGGGGA								1135
QY	1325	GATGATGGGGGCTTTAAATTTCCCAATGCTAAACAAATGAGAGAGGGGAAAGGGC								1384
Db	1136	GATGATGGGGGCTTTAAATTTCCCAATGCTAAACAAATGAGAGAGGGGAAAGGGC								1199
QY	1385	ACTATGGTTTATATTTTATATATTTTCGCTGCTGCTGCTGCTGATGAGCTTATGAT								1444
Db	1196	ACTATGGTTTATATTTTATATATTTTCGCTGCTGCTGCTGCTGATGAGCTTATGAT								1255
QY	1445	CTTTCCTTTCCTTTCTTTTGTGGGTAGAAATTGAATCCCTCAGCATTTTTCATCGTAGTTT								1504
Db	1256	CTTTCCTTTCCTTTCTTTTGTGGGTAGAAATTGAATCCCTCAGCATTTTTCATCGTAGTTT								1315
QY	1505	TTCTTTTCATGATTTTGACAAAGGAGCCCTCGGCGGAGCTTTTCTTAGTGTAGA								1560
Db	1316	TTCTTTTCATGATTTTGACAAAGGAGCCCTCGGCGGAGCTTTTCTTAGTGTAGA								1371
RESULT 7										
AAAT80052										
ID	AAAT80052 standard; cDNA; 2199 BP.									
XX										
AC	AAAT80052;									
XX										
DT	25-MAR-2003 (revised)									
DT	04-NOV-1997 (first entry)									
XX										
DE	Rice actin 1 gene promoter region.									
XX										
KM	Promoter; rice; actin 1 gene; cytoplasm; cytoskeleton; extension growth;									
KM	cytoplasmic streaming; cell division; Rac1; maize; Adh1 promoter; ss.									
XX										
OS	Oryza sativa.									
XX										
PN	US5641876-A.									
XX										
PD	24-JUN-1997.									
XX										
FX	27-OCT-1993; 93US-00144602.									
XX										
PR	05-JAN-1990; 90US-00461490.									
PR	18-SEP-1991; 91US-00762680.									
XX										
PA	(CORR) CORNELL RES FOUND INC.									
XX										
PI	Wu R, Mcelroy D;									
XX										

[illegible]

i

XX (GEMV) GENENCOR INT INC.
XX
XX Dunn-Coleman N, Langdon T, Morris P;
XX WPI; 2003-457563/43.
XX
XX New transgenic plant comprising an expression cassette with a promoter
PT operably linked to a ferulic acid esterase encoding polynucleotide, useful
PT for enhancing availability of fermentable carbohydrates as feed for grass
PT -fed animals.
XX
XX PS Disclosure; Fig 50; 190pp; English.
XX
XX The present invention relates to transgenic plants comprising an
CC expression cassette having a promoter operably linked to a ferulic acid
CC esterase (FAE) encoding polynucleotide. The transgenic plants are useful
CC for enhancing the availability of fermentable carbohydrates as feed for
CC grass-fed animals. The methods are useful for reducing the levels of
CC phenolic acids in the cell walls available for cross-linking either by
CC directly disrupting ester bonds linking phenolics and lignins to cell
CC wall polysaccharides or by preventing excessive fermentation of cell wall
CC carbohydrates. The present sequence was used to illustrate the invention.
XX
SQ Sequence 1259 BP; 337 A; 332 C; 268 G; 322 T; 0 U; 0 Other;

Query Match 15.1%; Score 236; DB 11; Length 1259;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1069 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTACACACCCGCTCTCTCTTTTC 1128
DB 896 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTACACACCCGCTCTCTCTTTTC 955
QY 1129 TTCTCCGTTTCTTTTTCGTCGATCTTGGCTTGGTGGTGGCG 1188
DB 956 TTCTCCGTTTCTTTTTCGTCGATCTTGGCTTGGTGGTGGCG 1015
QY 1189 AGAGCGGCTTCGTCGCGCCAGATCGTGCAGGAGGCGGAGTCTCGCGCTGCGCTCT 1248
DB 1016 AGAGCGGCTTCGTCGCGCCAGATCGTGCAGGAGGCGGAGTCTCGCGCTGCGCTCT 1075
QY 1249 CCGGCGCTGATGCGCGCGCGGATCTCGCGGGAATGGGGCTTCGATGTAGATCT 1304
DB 1076 CCGGCGCTGATGCGCGCGCGGATCTCGCGGGAATGGGGCTTCGATGTAGATCT 1131

RESULT 13
ADG69892
ID ADG69892 standard; DNA; 3657 BP.
XX
XX AC ADG69892;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Vector pTP8-5 nucleotide sequence.
XX
XX transgenic plant; ferulic acid esterase; FAE; enzyme; phenolic acid;
KM plant; cell wall; improved digestibility; biomass conversion;
KM highly fermentable carbohydrate; gene; ds.
XX
XX OS Synthetic.
XX
XX PN WO20026666-A1.
XX
XX PD 06-SEP-2002.
XX
XX PF 16-NOV-2001; 2001WO-US043588.
XX
XX PR 17-NOV-2000; 2000US-0249608P.
XX
XX PA (GEMV) GENENCOR INT INC.

PI Dunn-Coleman N, Langdon T, Morris P;
XX
XX DR WPI; 2002-698675/75.
XX P-PSDB; ADG69893.
XX
XX New transgenic plant comprising an expression cassette with a promoter
PT operably linked to a ferulic acid esterase encoding polynucleotide,
PT useful in improving digestibility for livestock and enhancing biomass
PT conversion.
XX
XX PS Disclosure; Fig 36B-E; 208pp; English.
XX
XX The present invention describes a transgenic plant (I) comprising an
CC expression cassette with a promoter operably linked to a ferulic acid
CC esterase encoding polynucleotide. Also described: (1) controlling (M1)
CC the level of phenolic acids in plant cell walls of a transgenic plant by
CC introducing into the plant an expression cassette comprising a promoter
CC operably linked to a ferulic acid esterase encoding polynucleotide; and
CC (2) a transgenic plant (II) produced by (M1). The transgenic plants are
CC useful in improving digestibility for livestock and enhancing biomass
CC conversion. The method is useful for enhancing the production of more
CC highly fermentable carbohydrates in plants, especially forage grasses.
CC The expression cassette is useful for controlling the level of phenolic
CC acids in plant cell walls of a transgenic plant. The present sequence is
CC used in the exemplification of the present invention.
XX
SQ Sequence 3657 BP; 916 A; 1012 C; 868 G; 860 T; 0 U; 1 Other;

Query Match 15.1%; Score 236; DB 6; Length 3657;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1069 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTACACACCCGCTCTCTTTTC 1128
DB 3310 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTACACACCCGCTCTCTTTTC 3369
QY 1129 TTCTCCGTTTCTTTTTCGTCGATCTTGGCTTGGTGGTGGCG 1188
DB 3370 TTCTCCGTTTCTTTTTCGTCGATCTTGGCTTGGTGGTGGCG 3429
QY 1189 AGAGCGGCTTCGTCGCGCCAGATCGTGCAGGAGGCGGAGTCTCGCGCTGCGCTCT 1248
DB 3430 AGAGCGGCTTCGTCGCGCCAGATCGTGCAGGAGGCGGAGTCTCGCGCTGCGCTCT 3489
QY 1249 CCGGCGCTGATGCGCGCGCGGATCTCGCGGGAATGGGGCTTCGATGTAGATCT 1304
DB 3490 CCGGCGCTGATGCGCGCGCGGATCTCGCGGGAATGGGGCTTCGATGTAGATCT 3545

RESULT 14
ADG69905
ID ADG69905 standard; DNA; 4604 BP.
XX
XX AC ADG69905;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Vector pPQ10.1 nucleotide sequence.
XX
XX transgenic plant; ferulic acid esterase; FAE; enzyme; phenolic acid;
KM plant; cell wall; improved digestibility; biomass conversion;
KM highly fermentable carbohydrate; gene; ds.
XX
XX OS Synthetic.
XX
XX PN WO20026666-A1.
XX
XX PD 06-SEP-2002.
XX
XX PF 16-NOV-2001; 2001WO-US043588.
XX
XX PR 17-NOV-2000; 2000US-0249608P.

```
PA (GENEV ) GENENCOR INT INC.
XX
XX Dunn-Coleman N, Langdon T, Morris P;
XX WPI; 2002-698675/75.
XX
XX New transgenic plant comprising an expression cassette with a promoter
XX operably linked to a ferulic acid esterase encoding polynucleotide,
XX PT useful in improving digestibility for livestock and enhancing biomass
XX conversion.
XX
XX Disclosure; Fig 45B-H; 208pp; English.
XX
XX The present invention describes a transgenic plant (I) comprising an
XX expression cassette with a promoter operably linked to a ferulic acid
XX esterase encoding polynucleotide. Also described: (1) controlling (M1)
XX the level of phenolic acids in plant cell walls of a transgenic plant by
XX introducing into the plant an expression cassette comprising a promoter
XX operably linked to a ferulic acid esterase encoding polynucleotide; and
XX (2) a transgenic plant (II) produced by (M1). The transgenic plants are
XX useful in improving digestibility for livestock and enhancing biomass
XX conversion. The method is useful for enhancing the production of more
XX highly fermentable carbohydrates in plants, especially forage grasses.
XX The expression cassette is useful for controlling the level of phenolic
XX acids in plant cell walls of a transgenic plant. The present sequence is
XX used in the exemplification of the present invention.
XX
XX Sequence 4604 BP; 1161 A; 1222 C; 1117 G; 1104 T; 0 U; 0 Other;
XX
XX Query Match 15.1%; Score 236; DB 6; Length 4604;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-101;
XX Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1069 GAGCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCGCTCTCTTC 1128
XX |||||
XX DB 4254 GAGCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCGCTCTCTTC 4313
XX
XX QY 1129 TTCTCCGTTTCTTCTCGTCTCGATCTTGCGCTTGATTTGGGTGGCG 1188
XX |||||
XX DB 4314 TTCTCCGTTTCTTCTCGTCTCGATCTTGCGCTTGATTTGGGTGGCG 4373
XX
XX QY 1189 AGAGCGGCTTCTGTCGCCAGATCGGTGCGGAGGCGGAGATCTCGCGCTGCGCTCT 1248
XX |||||
XX DB 4374 AGAGCGGCTTCTGTCGCCAGATCGGTGCGGAGGCGGAGATCTCGCGCTGCGCTCT 4433
XX
XX QY 1249 CCGGCGGTAGTTCGCGCCGATCTCTCGCGGGAATGGGGCTCTCGGATGTAAATCT 1304
XX |||||
XX DB 4434 CCGGCGGTAGTTCGCGCCGATCTCTCGCGGGAATGGGGCTCTCGGATGTAAATCT 4489
XX
XX RESULT 15
XX ADG69901
XX ID ADG69901 standard; DNA; 4773 BP.
XX
XX AC ADG69901;
XX
XX XX 11-MAR-2004 (first entry)
XX
XX DE Vector pGT6 nucleotide sequence.
XX
XX transgenic plant; ferulic acid esterase; FAE; enzyme; phenolic acid;
XX KM plant; cell wall; improved digestibility; biomass conversion;
XX highly fermentable carbohydrate; gene; ds.
XX
XX OS Synthetic.
XX
XX PN WO20026866-A1.
XX
XX PD 06-SEP-2002.
XX
XX PF 16-NOV-2001; 2001WO-US043588.
XX
XX PR 17-NOV-2000; 2000US-0249608P.
```

```
XX
XX (GENEV ) GENENCOR INT INC.
XX
XX Dunn-Coleman N, Langdon T, Morris P;
XX WPI; 2002-698675/75.
XX
XX New transgenic plant comprising an expression cassette with a promoter
XX operably linked to a ferulic acid esterase encoding polynucleotide,
XX PT useful in improving digestibility for livestock and enhancing biomass
XX conversion.
XX
XX Disclosure; Fig 41B-H; 208pp; English.
XX
XX The present invention describes a transgenic plant (I) comprising an
XX expression cassette with a promoter operably linked to a ferulic acid
XX esterase encoding polynucleotide. Also described: (1) controlling (M1)
XX the level of phenolic acids in plant cell walls of a transgenic plant by
XX introducing into the plant an expression cassette comprising a promoter
XX operably linked to a ferulic acid esterase encoding polynucleotide; and
XX (2) a transgenic plant (II) produced by (M1). The transgenic plants are
XX useful in improving digestibility for livestock and enhancing biomass
XX conversion. The method is useful for enhancing the production of more
XX highly fermentable carbohydrates in plants, especially forage grasses.
XX The expression cassette is useful for controlling the level of phenolic
XX acids in plant cell walls of a transgenic plant. The present sequence is
XX used in the exemplification of the present invention.
XX
XX Sequence 4773 BP; 1185 A; 1300 C; 1172 G; 1116 T; 0 U; 0 Other;
XX
XX Query Match 15.1%; Score 236; DB 6; Length 4773;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-101;
XX Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1069 GAGCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCGCTCTCTTC 1128
XX |||||
XX DB 4423 GAGCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCGCTCTCTTC 4482
XX
XX QY 1129 TTCTCCGTTTCTTCTCGTCTCGATCTTGCGCTTGATTTGGGTGGCG 1188
XX |||||
XX DB 4483 TTCTCCGTTTCTTCTCGTCTCGATCTTGCGCTTGATTTGGGTGGCG 4542
XX
XX QY 1189 AGAGCGGCTTCTGTCGCCAGATCGGTGCGGAGGCGGAGATCTCGCGCTGCGCTCT 1248
XX |||||
XX DB 4543 AGAGCGGCTTCTGTCGCCAGATCGGTGCGGAGGCGGAGATCTCGCGCTGCGCTCT 4602
XX
XX QY 1249 CCGGCGGTAGTTCGCGCCGATCTCTCGCGGGAATGGGGCTCTCGGATGTAAATCT 1304
XX |||||
XX DB 4603 CCGGCGGTAGTTCGCGCCGATCTCTCGCGGGAATGGGGCTCTCGGATGTAAATCT 4658
XX
```

Search completed: September 12, 2005, 09:45:30
Job time : 898.833 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 05:47:04 ; Search time 6651.44 Seconds
(without alignments)
8956.038 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565
1 GAATTCCTGCAGGTCCAGCG.....TTTTTGTAGTACGACCAG 1565

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	4.6	542	5 BQ609717	BQ609717 BRX_5803
2	55	3.5	293	8 CC001894	CC001894 PUBEC30TD
3	51	3.3	167	2 BE511568	BE511568 PUBC6G11
4	51	3.3	349	6 CA617416	CA617416 wlin.pk00
5	51	3.3	453	6 CA624228	CA624228 wlin.pk01
6	51	3.3	457	6 CA623099	CA623099 wlin.pk01
7	51	3.3	522	6 CA626045	CA626045 wlin.pk01
8	51	3.3	551	7 CO532828	CO532828 3530.1 21
9	51	3.3	560	2 BE510680	BE510680 946054G04
10	51	3.3	585	6 CA832049	CA832049 111702780
11	51	3.3	643	6 CA620555	CA620555 wlin.pk00
12	51	3.3	660	6 BU572118	BU572118 946168B10
13	50	3.2	629	5 BU499258	BU499258 946173D07
14	47	3.0	840	9 BU499363	BU499363 946174D07
15	46	2.9	731	7 CO528948	CO528948 3530.1 19
16	43	2.7	572	8 BZ541879	BZ541879 OGAJUD04TM
17	43	2.7	605	5 BQ744771	BQ744771 946111B02
18	43	2.7	697	8 BZ309389	BZ309389 1c06e11.b
19	43	2.7	729	9 CC676920	CC676920 OGVFS50TV
20	43	2.7	731	8 BZ324201	BZ324201 1c06e11.9
21	43	2.7	884	9 CG057952	CG057952 OGRBK17TV
22	43	2.7	840	8 CG057952	CG057952 PUDDK77TD
23	42	2.7	445	5 BQ744809	BQ744809 946111D08
24	42	2.7	520	8 CC044053	CC044053 3591_1_16

c	25	42	2.7	653	8 BH808262	BH808262 100807880
	26	42	2.7	795	6 CD437903	CD437903 E01N0506
	27	42	2.7	825	9 CG117429	CG117429 EPTCC12TB
	28	42	2.7	861	6 CD437683	CD437683 E01N0503
	29	41	2.6	716	8 BZ810022	BZ810022 PUGER46TD
	30	40	2.6	863	9 CC734241	CC734241 OGAO18TH
	31	40	2.6	906	9 CC734242	CC734242 OGAO18TH
c	32	39	2.5	790	8 BZ985422	BZ985422 PUG1227TD
	33	38	2.4	574	8 BH787841	BH787841 T2MB020TD
	34	38	2.4	668	5 BU079606	BU079606 946145G02
c	35	36	2.3	896	8 CC359562	CC359562 PUCB66TD
	36	35	2.3	954	8 CC359558	CC359558 PUCB66TD
	37	35	2.2	252	8 BH220473	BH220473 1006094G0
	38	35	2.2	254	8 BZ755321	BZ755321 PUPED87TB
	39	35	2.2	526	4 B1417123	B1417123 949053D12
c	40	35	2.2	526	4 B1674155	B1674155 949053D12
	41	35	2.2	639	8 BZ755322	BZ755322 PUPED87TD
c	42	35	2.2	771	8 BZ751817	BZ751817 PUDCT19TB
	43	35	2.2	771	8 BZ751819	BZ751819 PUDCT19TD
	44	35	2.2	785	8 BZ987838	BZ987838 PUDF850TD
	45	35	2.2	786	9 CG175670	CG175670 PUBJ35TD

ALIGNMENTS

RESULT 1
BQ609717 542 bp mRNA linear EST 25-JUN-2002
LOCUS BRX_5803 wheat EST endosperm library Triticum aestivum cDNA 5',
DEFINITION
BQ609717 BQ609717.1 GI:21559056
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 542)
REFERENCE
Clarke,B., Lambrecht,M. and Rhee,S.Y.
Arabidopsis genomic information for interpreting wheat EST
sequences
JOURNAL
TITLE
AUTHORS
MEDLINE
PUBMED
COMMENT
Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.
Location/Qualifiers
1..542
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wyuna"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/clone_lib="wheat EST endosperm library"

ORIGIN

Query Match 4.6% Score 72; DB 5; Length 542;
Best Local Similarity 100.0%; Pred. NO. 4.1e-26;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1347 CGCCAGCTTAACACAGATCAGGAAGGGAAGGCACTATGCTTATATTTTATAT 1406
DB 148 CGCCAGCTTAACACAGATCAGGAAGGGAAGGCACTATGCTTATATTTTATAT 207

QY 1407 ATTCTGCTGCT 1418
 |||||
 Db 208 ATTCTGCTGCT 219

RESULT 2
 CC001894
 LOCUS 293 bp DNA linear GSS 31-MAR-2003
 DEFINITION PUB0307D_ZM_0_6_1_0_KB Zea mays genomic clone ZMBR196E11,
 genomic survey sequence.
 ACCESSION CC001894
 VERSION CC001894.1 GI:29380454
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 293)
 Whitefaw,C.A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Resnick,A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Bernstzen,J.
 Maize Genomics Consortium
 Unpublished (2003)
 COMMENT Contact: Cathy Whitelaw
 TIGR
 912 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitefaw@tigr.org
 Seq primer: TP
 Class: sheared ends.

FEATURES
 source
 Location/Qualifiers
 1..293
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_lib="ZMBR196E11"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
 Cor selected genomic DNA library"

ORIGIN
 Query Match 3.5%; Score 55; DB 8; Length 293;
 Best Local Similarity 100.0%; Pred.No. 4.2e-17;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 819 ACCGGATCGCTCCCTACGCTTCACCTCATCGGCGCGCTCCATCTCCATCCACA 873
 |||||
 Db 208 ACCGGATCGCTCCCTACGCTTCACCTCATCGGCGCGCTCCATCTCCATCCACA 262

RESULT 3
 BS511568
 LOCUS 167 bp mRNA linear EST 07-AUG-2000
 DEFINITION 946061G11.y1 946 - tassels primordium prepared by Schmidt lab Zea
 mays cDNA, mRNA sequence.
 ACCESSION BS511568
 VERSION BS511568.1 GI:9732816
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 167)
 Walbot,V
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences

Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946061 row: G column: 11.
 Location/Qualifiers
 1..167
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to
 inflorescence development"
 /lab_host="Y10LR"
 /clone_lib="946 - tassels primordium prepared by Schmidt
 lab"
 /note="Organ: tassels; Vector: HybridZAP; Site_1: EcoRI;
 Site_2: XhoI; George Chuck dissected immature tassels
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybridZAP. Sample insert size range was 350 bp
 to 3 Kb with a 1 Kb average."

ORIGIN
 Query Match 3.3%; Score 51; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred.No. 5.6e-15;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CCCAATTCACGCTGCACCAACTGCGCTCTCCGCGCAGACCAAGA 1047
 |||||
 Db 2 CCCAATTCACGCTGCACCAACTGCGCTCTCCGCGCAGACCAAGA 52

RESULT 4
 CA617416
 LOCUS 349 bp mRNA linear EST 23-NOV-2002
 DEFINITION w1ln.pk0018.c3 w1ln Triticum aestivum cDNA clone w1ln.pk0018.c3 5'
 end, mRNA sequence.
 ACCESSION CA617416
 VERSION CA617416.1 GI:25195713
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Triticum.
 1 (bases 1 to 349)
 Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
 Miao,G., Caraher,N. and Hanafey,M.K.
 Dupont Wheat cDNA Sequence
 Unpublished (2002)
 COMMENT Contact: Scott V. Tingey
 Crop Genetics
 E. I. Dupont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingey@usa.dupont.com
 Seq primer: M13.
 Location/Qualifiers
 1..349
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone_lib="w1ln.pk0018.c3"
 /tissue_type="leaf"
 /clone_lib="w1ln"
 /note="Vector: pBluescript SK+, Site_1: EcoRI, Site_2:
 XhoI; wheat (Triticum aestivum L.) leaf 7 day old
 seedling, light grown (normalized)";

ORIGIN

Query Match 3.3%; Score 51; DB 6; Length 349;
 Best Local Similarity 100.0%; Pred. No. 5.5e-15;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 997 CCCAATTCCAGCTGCGCACCACTCGCGCTCTCCGCCAGACCAAGAAG 1047
 |||||
 17 CCCAATTCCAGCTGCGCACCACTCGCGCTCTCCGCCAGACCAAGAAG 67

RESULT 5
 CA624228 453 bp mRNA linear EST 23-NOV-2002
 LOCUS wlin.pk0138.e1 wlin Triticum aestivum cDNA clone wlin.pk0138.e1 5'
 DEFINITION end, mRNA sequence.
 ACCESSION CA624228
 VERSION CA624228.1 GI:25202524
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Triticum.
 1 (bases 1 to 453)
 Tingley, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
 Miao, G., Caraher, N. and Hanafey, M.K.
 Dupont Wheat cDNA Sequence
 Unpublished (2002)
 Contact: Scott V. Tingley
 Crop Genetics
 E. I. Dupont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2607
 Fax: 302-631-2607
 Email: Scott.V.Tingley@USA.dupont.com
 Seq primer: M13.
 Location/Qualifiers
 1..453
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wlin.pk0138.e1"
 /issue_type="leaf"
 /clone_lib="wlin"
 /note=Vector: pBluescript SK+, Site_1: EcoRI, Site_2:
 XhoI; wheat (Triticum aestivum L.) leaf 7 day old
 seedling, light grown (normalized)"

ORIGIN
 Query Match 3.3%; Score 51; DB 6; Length 453;
 Best Local Similarity 100.0%; Pred. No. 5.5e-15;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 997 CCCAATTCCAGCTGCGCACCACTCGCGCTCTCCGCCAGACCAAGAAG 1047
 |||||
 10 CCCAATTCCAGCTGCGCACCACTCGCGCTCTCCGCCAGACCAAGAAG 60

RESULT 6
 CA623099 457 bp mRNA linear EST 23-NOV-2002
 LOCUS wlin.pk0090.d12 wlin Triticum aestivum cDNA clone wlin.pk0090.d12
 DEFINITION 5' end, mRNA sequence.
 ACCESSION CA623099
 VERSION CA623099.1 GI:25201395
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Triticum.
 1 (bases 1 to 457)
 Tingley, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
 Miao, G., Caraher, N. and Hanafey, M.K.

REFERENCE
 AUTHORS

TITLE Dupont Wheat cDNA Sequence
 JOURNAL Unpublished (2002)
 COMMENT Contact: Scott V. Tingley
 Crop Genetics
 E. I. Dupont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2607
 Fax: 302-631-2607
 Email: Scott.V.Tingley@USA.dupont.com
 Seq primer: M13.
 Location/Qualifiers
 1..457
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wlin.pk0090.d12"
 /issue_type="leaf"
 /clone_lib="wlin"
 /note=Vector: pBluescript SK+, Site_1: EcoRI, Site_2:
 XhoI; wheat (Triticum aestivum L.) leaf 7 day old
 seedling, light grown (normalized)"

ORIGIN
 Query Match 3.3%; Score 51; DB 6; Length 457;
 Best Local Similarity 100.0%; Pred. No. 5.5e-15;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 997 CCCAATTCCAGCTGCGCACCACTCGCGCTCTCCGCCAGACCAAGAAG 1047
 |||||
 12 CCCAATTCCAGCTGCGCACCACTCGCGCTCTCCGCCAGACCAAGAAG 62

RESULT 7
 CA626045 522 bp mRNA linear EST 23-NOV-2002
 LOCUS wlin.pk0138.b11 wlin Triticum aestivum cDNA clone wlin.pk0138.b11
 DEFINITION 5' end, mRNA sequence.
 ACCESSION CA626045
 VERSION CA626045.1 GI:25204341
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Triticum.
 1 (bases 1 to 522)
 Tingley, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
 Miao, G., Caraher, N. and Hanafey, M.K.
 Dupont Wheat cDNA Sequence
 Unpublished (2002)
 Contact: Scott V. Tingley
 Crop Genetics
 E. I. Dupont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2607
 Fax: 302-631-2607
 Email: Scott.V.Tingley@USA.dupont.com
 Seq primer: M13.
 Location/Qualifiers
 1..522
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wlin.pk0138.b11"
 /issue_type="leaf"
 /clone_lib="wlin"
 /note=Vector: pBluescript SK+, Site_1: EcoRI, Site_2:
 XhoI; wheat (Triticum aestivum L.) leaf 7 day old
 seedling, light grown (normalized)"

ORIGIN
 Query Match 3.3%; Score 51; DB 6; Length 522;
 Best Local Similarity 100.0%; Pred. No. 5.5e-15;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CCCAATTTCAGCGCTGCCACCAACTGCGCGCTCCGCGCAAGCACAAG 1047
 |||
 12 CCCAATTTCAGCGCTGCCACCAACTGCGCGCTCCGCGCAAGCACAAG 62

RESULT 8
 COS32828 551 bp mRNA 1linear EST 15-JUL-2004
 LOCUS 3530_1.216.1.A05.V.1.3530 - Full length cDNA library created by
 In vitro from multiple tissues Zea mays cDNA, mRNA sequence.

ACCESSION
 COS32828
 VERSION COS32828.1 GI:50337702
 KEYWORDS EST.

SOURCE
 Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
 1 (bases 1 to 551)
 Malbot, V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 CONTACT: Malbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 3530.1.216.1 row: A column: 05.

FEATURES
 source
 1..551
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="multiple"
 /dev_stage="varies by tissue"
 /lab_host="DH10B"
 /clone_lib="3530 - Full length cDNA library created by
 In vitro from multiple tissues"
 /note="Organ: silks, husks, ears, pollen, shoot tips,
 leaf, root tips, whole seed, embryo; Vector: pCMV-SORT
 6.1; Site_1: EcoRV; Site_2: NotI; Maize Gene Discovery
 Project contracted with Invitrogen to produce a
 normalized, full length library in a pSport vector. This
 is a Gateway compatible vector, permitting clone movement
 to new vector backbones for expression in diverse host
 cells using recombination rather than restriction enzymes.
 Details of the vector and sequencing primers are available
 at ZmDB in the EST library description tables. poly(A)+
 RNA was prepared by Invitrogen, and equimolar amounts of
 RNA from each of the 12 tissue samples were mixed together
 for selection of mRNA with a 5' cap. After synthesis of
 cDNA, a normalization step was conducted against the
 mixture of RNA sources. This step effected a 20X to 80X
 reduction in common transcript types. Tissues prepared: 1.
 just emerging silks; 2. inner husks from ears of sample
 #1; 3. 20 day aleurone; 4. immature tassels, stages from
 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
 vegetative shoot tips from 15 day old seedlings; all
 leaves with an expanded or partially expanded sheath
 were removed; 8. mature leaf tissue; 9. 0.5 cm long root
 tips from 15 day old seedlings; 10. 10 day whole seed; 11.
 12 day endosperm and embryo; 12. 17 day endosperm and
 embryo. All of the sequenced clones in project 3530 will
 be archived at the University of Arizona along with the
 Unigene clones from the Maize Gene Discovery EST
 sequencing projects. Clones can be ordered through the
 ZmDB web site or directly from the University of Arizona

(http://www.genome.arizona.edu/orders/). High density
 filters containing over 18,000 clones can also be ordered
 from the University of Arizona."

ORIGIN

Query Match 3.3%; Score 51; DB 7; Length 551;
 Best Local Similarity 100.0%; Pred. No. 5.5e-15;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CCCAATTTCAGCGCTGCCACCAACTGCGCGCTCCGCGCAAGCACAAG 1047
 |||
 18 CCCAATTTCAGCGCTGCCACCAACTGCGCGCTCCGCGCAAGCACAAG 68

RESULT 9
 BE510680 560 bp mRNA 1linear EST 07-AUG-2000
 LOCUS 946054G04.Y1.946 - tassel primordium prepared by Schmidt lab Zea
 mays cDNA, mRNA sequence.

ACCESSION
 BE510680
 VERSION BE510680.1 GI:9731928
 KEYWORDS EST.

SOURCE
 Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
 1 (bases 1 to 560)
 Malbot, V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 CONTACT: Malbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946054 row: G column: 04.

FEATURES
 source
 1..560
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to
 inflorescence development"
 /lab_host="XL01R"
 /clone_lib="946 - tassel primordium prepared by Schmidt
 lab"
 /note="Organ: tassels; Vector: HybridZAP; Site_1: EcoRI;
 Site_2: XhoI; George Chuck dissected immature tassels
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybridZAP. Sample insert size range was 350 bp
 to 3 Kb with a 1 Kb average."

ORIGIN

Query Match 3.3%; Score 51; DB 2; Length 560;
 Best Local Similarity 100.0%; Pred. No. 5.4e-15;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CCCAATTTCAGCGCTGCCACCAACTGCGCGCTCCGCGCAAGCACAAG 1047
 |||
 2 CCCAATTTCAGCGCTGCCACCAACTGCGCGCTCCGCGCAAGCACAAG 52

RESULT 10
 CA832049 585 bp mRNA 1linear EST 12-DEC-2002
 LOCUS 111027B07.Y1.1117 - Unigene V from Maize Genome Project Zea mays
 cDNA, mRNA sequence.

ACCESSION CA832049
VERSION CA832049.1 GI:26559814
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS 1 (bases 1 to 585)
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 117027 row: B column: 07.
Location/Qualifiers
1. .585
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_id="1117 - Unigene V from Maize Genome Project"
/note="This library represents the unique genes found in the fifth round of EST sequencing at Stanford University for the maize genome project. Sequences are present from library 946. Contigs were assembled using ZmDBAssembler and 2 representatives from each contig were selected for the Unigene set. All singlets were also selected."

ORIGIN
Query Match 3.3%; Score 51; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CCCAATTCCACGCTGCACCACTCGCGTCTCCGCGCCAGACCAAG 1047
|||||
Db 13 CCCAATTCCACGCTGCACCACTCGCGTCTCCGCGCCAGACCAAG 63

RESULT 11
CA620555 643 bp mRNA linear EST 23-NOV-2002
LOCUS wlin.pk0056.d1 wlin Triticum aestivum cDNA clone wlin.pk0056.d1 5'
DEFINITION end, mRNA sequence.
ACCESSION CA620555
VERSION CA620555.1 GI:25198851
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.
AUTHORS 1 (bases 1 to 643)
Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.
TITLE Dupont Wheat cDNA Sequence
JOURNAL Unpublished (2002)
COMMENT Contact: Scott V. Tingey
Crop Genetics
B. I. Dupont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
Location/Qualifiers
1. .643
/organism="Triticum aestivum"

FEATURES
source

/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_id="wlin.pk0056.d1"
/issue_type="leaf"
/clone_id="wlin"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: XhoI; Wheat (Triticum aestivum L.) leaf 7 day old seedling, light grown (normalized)"

ORIGIN
Query Match 3.3%; Score 51; DB 6; Length 643;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CCCAATTCCACGCTGCACCACTCGCGTCTCCGCGCCAGACCAAG 1047
|||||
Db 18 CCCAATTCCACGCTGCACCACTCGCGTCTCCGCGCCAGACCAAG 68

RESULT 12
BU572118 660 bp mRNA linear EST 16-SEP-2002
LOCUS 946168B10.y1 946 - tassels primordium prepared by Schmidt lab Zea
DEFINITION mays cDNA, mRNA sequence.
ACCESSION BU572118 GI:22935843
VERSION BU572118.1
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS 1 (bases 1 to 660)
Walbot, V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946168 row: B column: 10.
Location/Qualifiers
1. .660
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/issue_type="tassels"
/dev_stage="Just after the transition from vegetative to inflorescence development"
/lab_note="XHOI"
/clone_id="946 - tassels primordium prepared by Schmidt lab"
/note="Organ: tassels; Vector: HybridZAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

ORIGIN
Query Match 3.3%; Score 51; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 CCCAATTCCACGCTGCACCACTCGCGTCTCCGCGCCAGACCAAG 1047
|||||
Db 15 CCCAATTCCACGCTGCACCACTCGCGTCTCCGCGCCAGACCAAG 65

FEATURES
source

RESULT 13
 BU499258 629 bp mRNA linear EST 12-SEP-2002
 LOCUS 946173D07.y1 946 - tassels primordium prepared by Schmidt lab Zea
 DEFINITION
 BU499258
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 629)
 Walbot,V
 Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL
 COMMENT
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946173 row: D column: 07.

FEATURES
 source
 1..629
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to inflorescence development"
 /lab_host="XL0LR"
 /clone_1lb="946 - tassels primordium prepared by Schmidt lab"
 /note="Organ: tassels; Vector: HybridZAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

ORIGIN
 Query Match 3.2%; Score 50; DB 5; Length 629;
 Best Local Similarity 100.0%; Pred. No. 1.8e-14;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 998 CCAATTCACGCTGCCACCACTCGCGCTCTCGCGCCAGCACAAG 1047
 Db 1 CCAATTCACGCTGCCACCACTCGCGCTCTCGCGCCAGCACAAG 50

RESULT 14
 BU499363 586 bp mRNA linear EST 12-SEP-2002
 LOCUS 946174D07.y1 946 - tassels primordium prepared by Schmidt lab Zea
 DEFINITION
 BU499363
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 586)
 Walbot,V
 Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL
 COMMENT
 Contact: Walbot V

Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946174 row: D column: 07.

FEATURES
 source
 1..586
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to inflorescence development"
 /lab_host="XL0LR"
 /clone_1lb="946 - tassels primordium prepared by Schmidt lab"
 /note="Organ: tassels; Vector: HybridZAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

ORIGIN
 Query Match 3.0%; Score 47; DB 5; Length 586;
 Best Local Similarity 100.0%; Pred. No. 7.1e-13;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1001 ATTCACGCTGCCACCACTCGCGCTCTCGCGCCAGCACAAG 1047
 Db 1 ATTCACGCTGCCACCACTCGCGCTCTCGCGCCAGCACAAG 47

RESULT 15
 COS28948 731 bp mRNA linear EST 15-JUL-2004
 LOCUS 3530_1.191.1.B09.y.1 3530 - Full length cDNA library created by Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
 DEFINITION
 3530_1.191.1.B09.y.1 3530 - Full length cDNA library created by Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 731)
 Walbot,V
 Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL
 COMMENT
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 3530_1.191.1 row: B column: 09.

FEATURES
 source
 1..731
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="multiple"
 /dev_stage="varies by tissue"
 /lab_host="DH10B"
 /clone_1lb="3530 - Full length cDNA library created by Invitrogen from multiple tissues"
 /note="Organ: silks, husks, ears, pollen, shoot tips,"

leaf, root tips, whole seed, embryo; Vector: PCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery Project contracted with Invitrogen to produce a normalized, full length library in a pSport vector. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the UniGene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

ORIGIN

Query Match 2.9%; Score 46; DB 7; Length 731;
 Best Local Similarity 100.0%; Pred. No. 2.4e-12;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1002 TTCCACGCTGCGACCAACTGCGCTCTCGCGCCAGACACCAAG 1047
 |||
 Db 34 TTCCACGCTGCGACCAACTGCGCTCTCGCGCCAGACACCAAG 79

Search completed: September 12, 2005, 14:04:13
 Job time : 6658.44 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 08:43:13 ; Search time 435.627 Seconds
(without alignments)
5878.368 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565
1 GAATTCCTGACGAGTCGACG.....TTTTTGTAGTAGACCAATG 1565

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/prodata/1/ina/PCOTUS.COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1565	100.0	1565	4 US-09-037-531-3	Sequence 3, Appl1
2	1021	65.2	1021	4 US-09-037-531-1	Sequence 1, Appl1
3	454	29.0	454	4 US-09-037-531-2	Sequence 2, Appl1
4	296	18.9	623	3 US-09-078-862-5	Sequence 5, Appl1
5	296	18.9	1392	1 US-08-144-602B-6	Sequence 6, Appl1
6	296	18.9	1404	1 US-08-144-602B-7	Sequence 7, Appl1
7	296	18.9	2199	1 US-08-144-602B-5	Sequence 5, Appl1
8	296	18.9	5643	1 US-08-144-602B-4	Sequence 4, Appl1
9	145	9.3	4032	3 US-09-068-101-5	Sequence 5, Appl1
10	145	9.3	4032	4 US-09-970-921-5	Sequence 5, Appl1
11	140	8.9	3039	4 US-09-377-466B-19	Sequence 19, Appl1
12	140	8.9	3039	4 US-09-377-466B-21	Sequence 21, Appl1
13	140	8.9	3044	4 US-09-377-466B-38	Sequence 38, Appl1
14	140	8.9	3450	4 US-09-377-466B-17	Sequence 17, Appl1
15	140	8.9	3455	4 US-09-377-466B-36	Sequence 36, Appl1
16	140	8.9	3469	4 US-09-377-466B-23	Sequence 23, Appl1
17	111	7.1	3694	3 US-09-080-625-5	Sequence 5, Appl1
18	111	7.1	3694	3 US-09-695-782-5	Sequence 5, Appl1
19	111	7.1	3877	3 US-09-080-625-4	Sequence 4, Appl1
20	111	7.1	3877	3 US-09-695-782-4	Sequence 4, Appl1
21	67	4.3	2107	3 US-09-441-340-29	Sequence 29, Appl1
22	67	4.3	2122	3 US-09-441-340-25	Sequence 25, Appl1
23	67	4.3	2378	3 US-09-441-340-27	Sequence 27, Appl1
24	27	1.7	4830	3 US-08-852-629-11	Sequence 11, Appl1
25	27	1.7	4838	3 US-08-852-629-15	Sequence 15, Appl1
26	24	1.5	144	4 US-09-702-705-1427	Sequence 1427, Ap
27	24	1.5	144	4 US-09-736-457-1427	Sequence 1427, Ap

28	24	1.5	144	4 US-09-614-124B-1427	Sequence 1427, Ap
29	24	1.5	144	4 US-09-671-325-1427	Sequence 1427, Ap
30	24	1.5	144	4 US-09-658-824-1427	Sequence 1427, Ap
31	24	1.5	190	4 US-09-702-705-1285	Sequence 1285, Ap
32	24	1.5	190	4 US-09-736-457-1285	Sequence 1285, Ap
33	24	1.5	190	4 US-09-614-124B-1285	Sequence 1285, Ap
34	24	1.5	190	4 US-09-671-325-1285	Sequence 1285, Ap
35	24	1.5	190	4 US-09-658-824-1285	Sequence 1285, Ap
36	23	1.5	34	4 US-09-914-397-10	Sequence 10, Appl1
37	23	1.5	40	3 US-09-065-058-5	Sequence 5, Appl1
38	23	1.5	53	3 US-08-974-549A-615	Sequence 615, App
39	23	1.5	53	4 US-09-402-181B-615	Sequence 615, App
40	23	1.5	53	4 US-09-721-456-615	Sequence 615, App
41	23	1.5	60	3 US-09-065-058-15	Sequence 15, Appl1
42	23	1.5	60	3 US-08-998-416-2	Sequence 2, Appl1
43	23	1.5	92	3 US-08-974-549A-614	Sequence 614, App
44	23	1.5	92	4 US-08-912-951-327	Sequence 327, App
45	23	1.5	92	4 US-09-402-181B-614	Sequence 614, App

ALIGNMENTS

RESULT 1

US-09-037-531-3

Sequence 3, Application US/09037531

Patent No. 6750378

GENERAL INFORMATION:

APPLICANT: Derose, Richard

TITLE OF INVENTION: Maize H3C4 Promoter Combined With The

TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSER: Connolly, Bove, Lodge, & Hutz

STREET: 1220 Market Street

CITY: Wilmington

STATE: DE

COUNTRY: USA

ZIP: 19899

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/037,531

FILING DATE: 10-MAR-1998

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: McMorrow Jr., Robert G.

REGISTRATION NUMBER: 30962

REFERENCE/DOCKET NUMBER: 5500*24

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302)658-9141

SEQUENCE CHARACTERISTICS:

LENGTH: 1565 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-037-531-3

Query Match 100.0% Score 1565; DB 4; Length 1565;
Best Local Similarity 100.0%; Pred No. 0;

Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCCTGACGAGTCGACGATCCCTTATGTGACCATTTACTGTAAATGCAATCAT 60
DB 1 GAATTCCTGACGAGTCGACGATCCCTTATGTGACCATTTACTGTAAATGCAATCAT 60

61 TTAATGAATAGCAACTTTTCTATTACTCTTACTTAACAATAATCTTGTTTAAAT 120
61 TTAATGAATAGCAACTTTTCTATTACTCTTACTTAACAATAATCTTGTTTAAAT 120
121 TCAGTCTCAACATTCATGCTCAAGATTAAGTTGAGCTGTCAAAATTTTAT 180
121 TCAGTCTCAACATTCATGCTCAAGATTAAGTTGAGCTGTCAAAATTTTAT 180
181 TTTCTATATTTTTTCTTATACATTTTGGGCTTACATTCATCTATATNCCA 240
181 TTTCTATATTTTTTCTTATACATTTTGGGCTTACATTCATCTATATNCCA 240
241 TCCCTTCCGGTGTCTCTAAAGATTCACCTCTGATCTTATCTCTCAATAAGT 300
241 TCCCTTCCGGTGTCTCTAAAGATTCACCTCTGATCTTATCTCTCAATAAGT 300
301 TCTCTAATCAGGTCTCTATAGCAATACTATATTAAGACATTTTTTATTTTGTAC 360
301 TCTCTAATCAGGTCTCTATAGCAATACTATATTAAGACATTTTTTATTTTGTAC 360
361 ATACATATTTGATCTCTCAATGATTAATACATATTTAGTTTACTTAAACGATAT 420
361 ATACATATTTGATCTCTCAATGATTAATACATATTTAGTTTACTTAAACGATAT 420
421 TTAAGTATTCAAACGAGTGAAGAACTGTTAGATAATTTCTATATATAGAAATCAGT 480
421 TTAAGTATTCAAACGAGTGAAGAACTGTTAGATAATTTCTATATATAGAAATCAGT 480
481 AGCGTTCTCTAAATTTAGATGATTTATTAAGAGACGCTGTTAGAAAAAGTAAATTCCT 540
481 AGCGTTCTCTAAATTTAGATGATTTATTAAGAGACGCTGTTAGAAAAAGTAAATTCCT 540
541 TTGATATTTATTTATTAAGGTAGAGTAAAGCTTTATGCTTATATGATCTTTGGGAGCCCA 600
541 TTGATATTTATTTATTAAGGTAGAGTAAAGCTTTATGCTTATATGATCTTTGGGAGCCCA 600
601 GCCTTATACCGGTATTTTGGCATTTGCGCTCTCATATTTCACTCCAGCGCCCAATTT 660
601 GCCTTATACCGGTATTTTGGCATTTGCGCTCTCATATTTCACTCCAGCGCCCAATTT 660
661 TCACGTTTTTCAACGAAAGCGCCAGCTGCTTAAACAAATTTGTTACGTTGCGCGGTT 720
661 TCACGTTTTTCAACGAAAGCGCCAGCTGCTTAAACAAATTTGTTACGTTGCGCGGTT 720
721 TTTCAAAAGAGTGGAAACCATCTGACCCACGACGATGAGGCGCTCGGATCTCTCCCTG 780
721 TTTCAAAAGAGTGGAAACCATCTGACCCACGACGATGAGGCGCTCGGATCTCTCCCTG 780
781 ATTAAGTCTAGGCAATAGAGCCAGAACCAACCATCAAGCGGATGCTCTTACGCTTC 840
781 ATTAAGTCTAGGCAATAGAGCCAGAACCAACCATCAAGCGGATGCTCTTACGCTTC 840
841 CACCTCATCGGCGCGCTCATCTTCATTCACCAACCTATTCGTTACCTTCCCATCTCC 900
841 CACCTCATCGGCGCGCTCATCTTCATTCACCAACCTATTCGTTACCTTCCCATCTCC 900
901 GAAAAAATTTCTGGCTCGCTCGCACTTACCAATTCATCCATCCATCAGACGAT 960
901 GAAAAAATTTCTGGCTCGCTCGCACTTACCAATTCATCCATCCATCAGACGAT 960
961 CGCATCACTGCAAAATCCCCCAAAAATCAACACCTCCCAATTCAGAGTCCACCAACT 1020
961 CGCATCACTGCAAAATCCCCCAAAAATCAACACCTCCCAATTCAGAGTCCACCAACT 1020
1021 CGCGTCTCTCGCGCCAGAACCAAAAGAAATGGCGCCACCGCGGTGAGACTCTTCCC 1080
1021 CGCGTCTCTCGCGCCAGAACCAAAAGAAATGGCGCCACCGCGGTGAGACTCTTCCC 1080
1081 CTTCCCTCTCGCGCGCGCGGTAAACACCCCGCTCTCTCTTCTTCTTCTCGGTTT 1140
1081 CTTCCCTCTCGCGCGCGCGGTAAACACCCCGCTCTCTCTTCTTCTTCTCGGTTT 1140
1141 TTTTTCGTCTCGGTCTCGATCTTTGGCTTGGATTTGGGTGGGAGAGGCGGCTTG 1200

1141 TTTTTCGTCTCGGTCTCGATCTTTGGCTTGGATTTGGGTGGGAGAGCGGCTTG 1200
1201 TGGCCAGATCGGTGCGGGAGGGGCGGGGATCTGCGGCTGGCGCTCCGGCGTGAAT 1260
1201 TGGCCAGATCGGTGCGGGAGGGGCGGGGATCTGCGGCTGGCGCTCCGGCGTGAAT 1260
1261 CGGCCGATCTCTCGCGGGGAATGGGGCTCTCGATGATCTGATCCGCGTTGTGG 1320
1261 CGGCCGATCTCTCGCGGGGAATGGGGCTCTCGATGATCTGATCCGCGTTGTGG 1320
1261 CGGCCGATCTCTCGCGGGGAATGGGGCTCTCGATGATCTGATCCGCGTTGTGG 1320
1321 GGGAGATGATGGGGCGTTTAAATTTGCGCATGCTTAAACAGATCAGAAAGGGGAAA 1380
1321 GGGAGATGATGGGGCGTTTAAATTTGCGCATGCTTAAACAGATCAGAAAGGGGAAA 1380
1381 GGGCATAGTGTATATTTTATATATTTGCTGCTGCTGCTGCTGAGGCTTATGTGCT 1440
1381 GGGCATAGTGTATATTTTATATATTTGCTGCTGCTGCTGCTGAGGCTTATGTGCT 1440
1441 AGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1500
1441 AGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1500
1501 GTTTTCTTTCATGATTTGTGACAAATGCAAGCTCTGCGGAGCTTTTGTAGGTAGA 1560
1501 GTTTTCTTTCATGATTTGTGACAAATGCAAGCTCTGCGGAGCTTTTGTAGGTAGA 1560
1561 CCATG 1565
1561 CCATG 1565

RESULT 2
US-09-037-531-1
; Sequence 1, Application US/09037531
; Patent No. 6750378
; GENERAL INFORMATION:
; APPLICANT: DeRose, Richard
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
; TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,531
; FILING DATE: 10-MAR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G.
; REGISTRATION NUMBER: 30962
; REFERENCE/DOCKET NUMBER: 5500*24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302)658-9141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1021 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-037-531-1

Query Match 65.2%; Score 1021; DB 4; Length 1021;
 Best Local Similarity 100.0%; Pred.No.0;
 Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 27 CTATGTGACCATTAATCTGTAATGCAATCAATTAATGATAGCAAACTTTCTATT 86
DB 1 CTATGTGACCATTAATCTGTAATGCAATCAATTAATGATAGCAAACTTTCTATT 60
QY 87 ACTTCTTTACTAAATTAATCTGTTTAAATTCAGTCTCAACATTCATTGCTCAAG 146
DB 61 ACTTCTTTACTAAATTAATCTGTTTAAATTCAGTCTCAACATTCATTGCTCAAG 120
QY 147 TATAAGTTGAGACTGTCMAAATTTACTATTATTTCTTATATTTTCTTATACA 206
DB 121 TATAAGTTGAGACTGTCMAAATTTACTATTATTTCTTATATTTTCTTATACA 180
QY 207 CATTTGGGCTTACATCATCATCATCATCATCATCATCATCATCATCATCATCAT 286
DB 181 CATTTGGGCTTACATCATCATCATCATCATCATCATCATCATCATCATCATCAT 240
QY 267 CCATCTCTGAAATCTTATCTCTCAATACGTTCTTAATCAGGTCCTATTAAGCA 326
DB 241 CCATCTCTGAAATCTTATCTCTCAATACGTTCTTAATCAGGTCCTATTAAGCA 300
QY 327 TACCTATATTAGAGACATTTTATTTTGTATATATATTTTGTATATCTCAATG 386
DB 301 TACCTATATTAGAGACATTTTATTTTGTATATATATTTTGTATATCTCAATG 360
QY 387 CATTAATACATTTAGTTTACTAAACCGATTTTAAATTTAAATTTAAAGGATGAAC 446
DB 361 CATTAATACATTTAGTTTACTAAACCGATTTTAAATTTAAATTTAAAGGATGAAC 420
QY 447 TGTTTAGATTAATTTCTATATATATAGAGATCCAGTAGCGTCTTAATTTAGATTA 506
DB 421 TGTTTAGATTAATTTCTATATATATAGAGATCCAGTAGCGTCTTAATTTAGATTA 480
QY 507 TTAGAGAGCGCTGTAGAAAACGTAAAAATCTTGATTTATTTATTTAGGATGAGT 566
DB 481 TTAGAGAGCGCTGTAGAAAACGTAAAAATCTTGATTTATTTATTTAGGATGAGT 540
QY 567 AGCCTTAAGCTTTATAGATCTTTGTGAGACCAAGCTTATACGGTATTTTCGGAT 626
DB 541 AGCCTTAAGCTTTATAGATCTTTGTGAGACCAAGCTTATACGGTATTTTCGGAT 600
QY 627 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCACTTTTCACTCCAGCGCCCAAG 686
DB 601 GCGCTCTCATTTTCACTCCAGCGCCCAATTTTCACTTTTCACTCCAGCGCCCAAG 660
QY 687 TGCCTAACCAAAATTTGTAGCGTGGCGGTTTCAAAAAGAAAGTGGAAACCATCTGC 746
DB 661 TGCCTAACCAAAATTTGTAGCGTGGCGGTTTCAAAAAGAAAGTGGAAACCATCTGC 720
QY 747 ACCCAGGATAGTAGGCGCTCGGATCTCTCGATTAATGCTTAGGCAATAGAGCCCA 806
DB 721 ACCCAGGATAGTAGGCGCTCGGATCTCTCGATTAATGCTTAGGCAATAGAGCCCA 780
QY 807 GAACACCCATCAAGCGGATCGTCCCTCAAGCTTCACTCATGCGGCGGCTCATCTCCA 866
DB 781 GAACACCCATCAAGCGGATCGTCCCTCAAGCTTCACTCATGCGGCGGCTCATCTCCA 840
QY 867 TCCAAACATTAATCGTTATCTTGCCATCTCCGAAAAAATTTCTGGGCTCGGCTCCG 926
DB 841 TCCAAACATTAATCGTTATCTTGCCATCTCCGAAAAAATTTCTGGGCTCGGCTCCG 900
QY 927 ACCTACTAGAAATACCATCCATCCATCAAGAGCATCGCATCACTGCAAAATCCCAAGAA 986
DB 901 ACCTACTAGAAATACCATCCATCCATCAAGAGCATCGCATCACTGCAAAATCCCAAGAA 960
QY 987 ATCAACACCTCCCAATTCAGGCTGCAACCAACTCGCGCTCTCGGCGCAACACCAAA 1046
DB 961 ATCAACACCTCCCAATTCAGGCTGCAACCAACTCGCGCTCTCGGCGCAACACCAAA 1020

```

QY 1047 G 1047
 DB 1021 G 1021

RESULT 3
 US-09-037-531-2
 ; Sequence 2, Application US/09037531
 ; Patent No. 6750378
 ; GENERAL INFORMATION:
 ; APPLICANT: Derose, Richard
 ; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
 ; TITLE OF INVENTION: First Inton Of Rice Actin, Chimeric Gene Comprising It
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
 ; STREET: 1220 Market Street
 ; CITY: Wilmington
 ; STATE: DE
 ; COUNTRY: USA
 ; ZIP: 19899
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/037,531
 ; FILING DATE: 10-MAR-1998
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMorrow Jr., Robert G.
 ; REGISTRATION NUMBER: 30962
 ; REFERENCE/DOCKET NUMBER: 5500*24
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (302)658-9141
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 454 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-09-037-531-2

Query Match 29.0%; Score 454; DB 4; Length 454;
 Best Local Similarity 100.0%; Pred.No.1.3e-211;
 Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1102 GTTACACCCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1161
DB 1 GTTACACCCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
QY 1162 CTTTGGCTTTGATGTTGGGTGGGAGAGCGGCTTCTCGCCAGATCGGCGGG 1221
DB 61 CTTTGGCTTTGATGTTGGGTGGGAGAGCGGCTTCTCGCCAGATCGGCGGG 120
QY 1222 AGGGGGGAGATCTCGGGGCTGCGCTCTCGGGGCTGAGTCCGCGCGGAGATCTCGGGGGA 1281
DB 121 AGGGGGGAGATCTCGGGGCTGCGCTCTCGGGGCTGAGTCCGCGCGGAGATCTCGGGGGA 180
QY 1282 ATGGGGCTCTCGGATAGATCGATCCGCGTTGTTGGGGAGATGATGAGGCGTTTAA 1341
DB 181 ATGGGGCTCTCGGATAGATCGATCCGCGTTGTTGGGGAGATGATGAGGCGTTTAA 240
QY 1342 AATTTGCCATGTAAACAAGATCAGAGAGAGGGGAAAAAGGCACTATGTTATTTT 1401
DB 241 AATTTGCCATGTAAACAAGATCAGAGAGAGGGGAAAAAGGCACTATGTTATTTT 300
QY 1402 TATATATTTCTGCTGCTCGTCAAGGCTTAGATGCTAGATCTTTCTTTCTTTT 1461

```

Db 301 TATATATTCGTGCTGCTGCTGACGCTTAGATGTGATCTTTCTTTCTTTT 360
QY 1462 GGGGGAGAAATTTGATCCCTCGATGTTGATCGTAGTTTCTTTTCAAGATTGT 1521
Db 361 GGGGGAGAAATTTGAAATCCCTCAGCAATGTTCACTGTTCTTTTCAAGATTGT 420
QY 1522 GACAAATGACCTCGTGGCGAGACTTTTGTAG 1555
Db 421 GACAAATGACCTCGTGGCGAGACTTTTGTAG 454

RESULT 4

US-09-078-862-5
; Sequence 5, Application US/09078862
; Patent No. 6091003
; GENERAL INFORMATION:
; APPLICANT: Nan, Guo-Ling
; APPLICANT: Nagai, Chifumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC
; TITLE OF INVENTION: TRANSFORMATION OF PINEAPPLE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/078,862
; FILING DATE: 14-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: US-03321
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 623 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-09-078-862-5

Query Match 18.9%; Score 296; DB 3; Length 623;

Best Local Similarity 100.0%; Pred. No. 2,2e-134; Indels 0; Gaps 0;

Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1265 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCGGCCGTTGTGGGGGA 1324
Db 278 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCGGCCGTTGTGGGGGA 337
QY 1325 GAGGATGGGCGCTTTAAATTTGGCCATGCTAAACAAGATCAGAAAGAGGGGAAAAGGC 1384
Db 338 GAGGATGGGCGCTTTAAATTTGGCCATGCTAAACAAGATCAGAAAGAGGGGAAAAGGC 397
QY 1385 ACTATGGTTATATTTTATATATTTCTGCTGCTCTGTCAGGCTTAGTGTAGAT 1444
Db 398 ACTATGGTTATATTTTATATATTTCTGCTGCTCTGTCAGGCTTAGTGTAGAT 457
QY 1445 CTTTCTTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCAATGTTTCAATGGGTAGTT 1504
Db 458 CTTTCTTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCAATGTTTCAATGGGTAGTT 517

QY 1505 TTCTTTTCATGATTTGTGACAAATGACAGCTGTCGGAGACTTTTGTAGGTAGA 1560
Db 518 TTCTTTTCATGATTTGTGACAAATGACAGCTGTCGGAGACTTTTGTAGGTAGA 573

RESULT 5

US-08-144-602B-6
; Sequence 6, Application US/08144602B
; Patent No. 5641876
; GENERAL INFORMATION:
; APPLICANT: McElroy, David
; APPLICANT: Wu, Ray
; TITLE OF INVENTION: RICE ACTIN GENE AND PROMOTER
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: CLINTON SQUARE, P.O. BOX 1051
; CITY: ROCHESTER
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,602B
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TIMIAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/10140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1600
; TELEFAX: 716-263-1636
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-144-602B-6

Query Match 18.9%; Score 296; DB 1; Length 1392;

Best Local Similarity 100.0%; Pred. No. 2,2e-134; Indels 0; Gaps 0;

Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1265 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCGGCCGTTGTGGGGGA 1324
Db 1076 CCGGATCTTCGCGGGGAATGGGCTCTCGGATGTAGATCGGCCGTTGTGGGGGA 1135
QY 1325 GATGATGGGCGCTTTAAATTTGGCCATGCTAAACAAGATCAGAAAGAGGGGAAAAGGC 1384
Db 1136 GATGATGGGCGCTTTAAATTTGGCCATGCTAAACAAGATCAGAAAGAGGGGAAAAGGC 1195
QY 1385 ACTATGGTTATATTTTATATATTTCTGCTGCTCTGTCAGGCTTAGATGTAGAT 1444
Db 1196 ACTATGGTTATATTTTATATATTTCTGCTGCTCTGTCAGGCTTAGATGTAGAT 1255
QY 1445 CTTTCTTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCAATGTTTCAATGGGTAGTT 1504
Db 1256 CTTTCTTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCAATGTTTCAATGGGTAGTT 1315
QY 1505 TTCTTTTCATGATTTGTGACAAATGACAGCTGTCGGAGACTTTTGTAGGTAGA 1560
Db 1316 TTCTTTTCATGATTTGTGACAAATGACAGCTGTCGGAGACTTTTGTAGGTAGA 1371

RESULT 6


```

; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,602B
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TIMIAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/10140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-144-602B-4

Query Match      18.9%; Score 296; DB 1; Length 5643;
Best Local Similarity 100.0%; Pred. No. 2.2e-134;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1265 CCGGATCTCCGCGGGAATGGGCTCTCGATGTAGATCCGCCGTTGTGGGGGA 1324
DB      1886 CCGGATCTCCGCGGGAATGGGCTCTCGATGTAGATCCGCCGTTGTGGGGGA 1945
QY      1325 GATGATGGGGCGTTTAAATTTGCGCATGCTTAAACAAGATCAGAGAGGGGAAAAGGCG 1384
DB      1946 GATGATGGGGCGTTTAAATTTGCGCATGCTTAAACAAGATCAGAGAGGGGAAAAGGCG 2005
QY      1385 ACTATGGTTATATTTTATATATTTCTGCTGCGCTCGTCAAGGCTTAGATGTAGAT 1444
DB      2006 ACTATGGTTATATTTTATATATTTCTGCTGCGCTCGTCAAGGCTTAGATGTAGAT 2065
QY      1445 CTTTCCTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTTGTTCAATCGTAGTT 1504
DB      2066 CTTTCCTTCTCTTTTGTGGGTAGAAATTTGAATCCCTCAGCATTTGTTCAATCGTAGTT 2125
QY      1505 TTCTTTTCATGATTTGTGACAAATGCAGCCTCGTGGGAGCTTTTGTAGGTAGA 1560
DB      2126 TTCTTTTCATGATTTGTGACAAATGCAGCCTCGTGGGAGCTTTTGTAGGTAGA 2181

RESULT 9
US-09-068-101-5
; Sequence 5, Application US/09068101
; Patent No. 6372960
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2121-139P
; CURRENT APPLICATION NUMBER: US/09/068,101
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: EP 9620244.9
; EARLIER FILING DATE: 1996-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pmv71"
; FEATURE:
```

```

; NAME/KEY: misc feature
; LOCATION: (1999)..(3400)
; OTHER INFORMATION: label = PRAcI, "promoter region of rice actin gene"
; OTHER INFORMATION: - contains an intron in the leader"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3401)..(3676)
; OTHER INFORMATION: label = barstar, "barstar DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3677)..(4003)
; OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
; OTHER INFORMATION: T-DNA"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3399)..(3404)
; OTHER INFORMATION: label = NcoI, "NcoI recognition site"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4016)..(4021)
; OTHER INFORMATION: label = KpnI, "KpnI recognition site"
; US-09-068-101-5

Query Match      9.3%; Score 145; DB 3; Length 4032;
Best Local Similarity 100.0%; Pred. No. 1.4e-60;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1421 TCGTAGGCTTGAGATGCTAGATCTTTCTTTCTTTTGGGTGAATTGAATCC 1480
DB      3259 TCGTAGGCTTGAGATGCTAGATCTTTCTTTCTTTTGGGTGAATTGAATCC 3318
QY      1481 CTCAGCATGTCATCGTAGTATTTCTTTTCATGATTTGTACAATGCAGCCTCGTGC 1540
DB      3319 CTCAGCATGTCATCGTAGTATTTCTTTTCATGATTTGTACAATGCAGCCTCGTGC 3378
QY      1541 GGAGCTTTTGTAGGTAGCCATG 1565
DB      3379 GGAGCTTTTGTAGGTAGCCATG 3403

RESULT 10
US-09-970-921-5
; Sequence 5, Application US/0970921
; Patent No. 6759575
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4032
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "plasmid pmv71"
; NAME/KEY: misc feature
; LOCATION: (1999)..(3400)
; OTHER INFORMATION: label = PRAcI, "promoter region of rice actin gene"
; OTHER INFORMATION: - contains an intron in the leader"
; NAME/KEY: misc feature
; LOCATION: (3401)..(3676)
; OTHER INFORMATION: label = barstar, "barstar DNA"
; NAME/KEY: misc feature
; LOCATION: (3677)..(4003)
; OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
; OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
; OTHER INFORMATION: T-DNA"
; NAME/KEY: misc feature
```

```
LOCATION: (3399)..(3404)
OTHER INFORMATION: label = NcoI, "NcoI recognition site"
NAME/KEY: misc_feature
LOCATION: (4016)..(4021)
OTHER INFORMATION: label = KpnI, "KpnI recognition site"
US-09-970-921-5
```

```
Query Match          9.3%; Score 145; DB 4; Length 4032;
Best Local Similarity 100.0%; Pred. No. 1.4e-60;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1421 TCCTCAGGCTTAGATGCTAGATCTTCTTCTTTGCGGTAGAAATTTGAATCC 1480
      |||
DB 3259 TCCTCAGGCTTAGATGCTAGATCTTCTTCTTTGCGGTAGAAATTTGAATCC 3318

QY 1481 CTCAGCATTTTCATCGGATGTTTCTTTTCATGATTTGTGACAAATGCGCTCGTGC 1540
      |||
DB 3319 CTCAGCATTTTCATCGGATGTTTCTTTTCATGATTTGTGACAAATGCGCTCGTGC 3378

QY 1541 GGAGCTTTTGTAGGTAGACCATG 1565
      |||
DB 3379 GGAGCTTTTGTAGGTAGACCATG 3403
```

```
RESULT 11
US-09-377-466B-19
Sequence 19, Application US/09377466B
Patent No. 6501009
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 3039
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
NAME/KEY: promoter
LOCATION: (14)..(235)
OTHER INFORMATION: P-CaMV.AS4
NAME/KEY: 5'UTR
LOCATION: (240)..(304)
OTHER INFORMATION: L-Ta.hcbl
NAME/KEY: Intron
LOCATION: (318)..(805)
OTHER INFORMATION: I-Os.Act1
NAME/KEY: CDS
LOCATION: (811)..(2769)
OTHER INFORMATION: Cry3Bb1 variant 11231mw1
NAME/KEY: terminator
LOCATION: (2787)..(3020)
OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-19
```

```
Query Match          8.9%; Score 140; DB 4; Length 3039;
Best Local Similarity 100.0%; Pred. No. 3.9e-58;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1421 TCCTCAGGCTTAGATGCTAGATCTTCTTCTTTGCGGTAGAAATTTGAATCC 1480
      |||
DB 660 TCCTCAGGCTTAGATGCTAGATCTTCTTCTTTGCGGTAGAAATTTGAATCC 719

QY 1481 CTCAGCATTTTCATCGGATGTTTCTTTTCATGATTTGTGACAAATGCGCTCGTGC 1540
      |||
DB 720 CTCAGCATTTTCATCGGATGTTTCTTTTCATGATTTGTGACAAATGCGCTCGTGC 779

QY 1541 GGAGCTTTTGTAGGTAGACCATG 1560
```

```
|||||
DB 780 GGAGCTTTTGTAGGTAGACCATG 799
```

```
RESULT 12
US-09-377-466B-21
Sequence 21, Application US/09377466B
Patent No. 6501009
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 3039
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
NAME/KEY: promoter
LOCATION: (14)..(235)
OTHER INFORMATION: P-CaMV.AS4
NAME/KEY: 5'UTR
LOCATION: (240)..(304)
OTHER INFORMATION: L-Ta.hcbl
NAME/KEY: Intron
LOCATION: (318)..(805)
OTHER INFORMATION: I-Os.Act1
NAME/KEY: CDS
LOCATION: (811)..(2769)
OTHER INFORMATION: Cry3Bb1 variant 11231mw2
NAME/KEY: terminator
LOCATION: (2787)..(3020)
OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-21
```

```
Query Match          8.9%; Score 140; DB 4; Length 3039;
Best Local Similarity 100.0%; Pred. No. 3.9e-58;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1421 TCCTCAGGCTTAGATGCTAGATCTTCTTCTTTGCGGTAGAAATTTGAATCC 1480
      |||
DB 660 TCCTCAGGCTTAGATGCTAGATCTTCTTCTTTGCGGTAGAAATTTGAATCC 719

QY 1481 CTCAGCATTTTCATCGGATGTTTCTTTTCATGATTTGTGACAAATGCGCTCGTGC 1540
      |||
DB 720 CTCAGCATTTTCATCGGATGTTTCTTTTCATGATTTGTGACAAATGCGCTCGTGC 779

QY 1541 GGAGCTTTTGTAGGTAGACCATG 1560
      |||
DB 780 GGAGCTTTTGTAGGTAGACCATG 799
```

```
RESULT 13
US-09-377-466B-38
Sequence 38, Application US/09377466B
Patent No. 6501009
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38
LENGTH: 3044
TYPE: DNA
ORGANISM: Artificial Sequence
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2005, 11:40:58 ; Search time 830.171 Seconds
(without alignments)
12380.260 Million cell updates/sec

Title: US-10-758-799-3

Perfect score: 1565
Sequence: 1 GAATTCCTCAGAGTCGACG.....TTTTTGTAGTAGACCAAG 1565

Scoring table: OLIGO NUC
Gap 60.0, Gapext 60.0

Searched: 7351250 seqs, 3283620254 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1565	100.0	1565	9	US-09-037-531-3
2	1565	100.0	1565	19	US-10-758-799-3
3	1021	65.2	1021	9	US-09-037-531-1
4	1021	65.2	1021	19	US-10-758-799-1
5	454	29.0	454	9	US-09-037-531-2
6	454	29.0	454	19	US-10-758-799-2
7	296	18.9	623	9	US-09-981-900B-19

8	294	18.8	470	16	US-10-087-167-109	Sequence 109, App
9	236	15.1	1259	10	US-09-991-209-43	Sequence 43, App1
10	236	15.1	4773	10	US-09-991-209-32	Sequence 32, App1
11	236	15.1	4950	10	US-09-991-209-34	Sequence 34, App1
12	236	15.1	4965	10	US-09-991-209-37	Sequence 37, App1
13	236	15.1	4974	10	US-09-991-209-35	Sequence 35, App1
14	236	15.1	5164	10	US-09-991-209-36	Sequence 36, App1
15	236	15.1	5277	10	US-09-991-209-25	Sequence 25, App1
16	236	15.1	5395	10	US-09-991-209-38	Sequence 38, App1
17	236	15.1	5327	10	US-09-991-209-27	Sequence 27, App1
18	236	15.1	5337	10	US-09-991-209-19	Sequence 19, App1
19	236	15.1	5337	10	US-09-991-209-23	Sequence 23, App1
20	236	15.1	5337	10	US-09-991-209-31	Sequence 31, App1
21	236	15.1	5338	10	US-09-991-209-15	Sequence 15, App1
22	236	15.1	5338	10	US-09-991-209-29	Sequence 29, App1
23	236	15.1	5345	10	US-09-991-209-17	Sequence 17, App1
24	236	15.1	5387	10	US-09-991-209-41	Sequence 41, App1
25	236	15.1	5395	10	US-09-991-209-21	Sequence 21, App1
26	145	9.3	2480	21	US-10-678-588A-1	Sequence 1, App1
27	145	9.3	4032	9	US-09-970-921-5	Sequence 5, App1
28	145	9.3	5365	22	US-10-833-092-57	Sequence 57, App1
29	145	9.3	7943	10	US-09-845-064-15	Sequence 15, App1
30	145	9.3	9143	10	US-09-845-064-12	Sequence 12, App1
31	145	9.3	10003	10	US-09-845-064-21	Sequence 21, App1
32	142	9.1	9359	21	US-10-344-977A-1	Sequence 1, App1
33	142	9.1	9359	22	US-10-344-975B-1	Sequence 1, App1
34	141	9.0	6865	10	US-09-845-064-13	Sequence 13, App1
35	141	9.0	10003	10	US-09-845-064-21	Sequence 21, App1
36	140	8.9	491	9	US-09-376-940-50	Sequence 50, App1
37	140	8.9	1597	22	US-10-833-092-50	Sequence 50, App1
38	140	8.9	3034	20	US-10-841-796-34	Sequence 34, App1
39	140	8.9	3039	15	US-10-232-665-17	Sequence 17, App1
40	140	8.9	3039	15	US-10-232-665-21	Sequence 21, App1
41	140	8.9	3444	15	US-10-232-665-38	Sequence 38, App1
42	140	8.9	3450	15	US-10-232-665-17	Sequence 17, App1
43	140	8.9	3455	15	US-10-232-665-36	Sequence 36, App1
44	140	8.9	3469	15	US-10-232-665-23	Sequence 23, App1
45	140	8.9	7794	24	US-11-057-062-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-09-037-531-3
; Sequence 3, Application US/09037531
; Patent No. US20020104117A1
GENERAL INFORMATION:
APPLICANT: DeRose, Richard
TITLE OF INVENTION: Freysinet, Georges
TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
TITLE OF INVENTION: And Transformed Plant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Connolly, Bove, Lodge, & Rutz
STREET: 1220 Market Street
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037, 531
FILING DATE: 10-MAR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McMorro Jr., Robert G.
REGISTRATION NUMBER: 30962

```
REFERENCE/DOCKET NUMBER: 5500*24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)658-9141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-037-531-3

Query Match      100.0%; Score 1565; DB 9; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCCTGACAGGTGACGAGATCCCTTATGTGACCAATTTACTGTAAATGCAATATCAT 60
DB 1 GAATTCCTGACAGGTGACGAGATCCCTTATGTGACCAATTTACTGTAAATGCAATATCAT 60
QY 61 TTAATTTGAATAGAACTTTTCTTATTAATCTTTTACTTAAATATTTCTGTGTTTAAAT 120
DB 61 TTAATTTGAATAGAACTTTTCTTATTAATCTTTTACTTAAATATTTCTGTGTTTAAAT 120
QY 121 TCAGTCTCAACATTCATTGCTCAAGTATATAGTTGAGACTGTCAAAATTTACTATTTTAT 180
DB 121 TCAGTCTCAACATTCATTGCTCAAGTATATAGTTGAGACTGTCAAAATTTACTATTTTAT 180
QY 181 TTCTTCATATTTTTTTTCTTATATACATATTTGGGCTTACAAATTCATCATCTATATTC 240
DB 181 TTCTTCATATTTTTTTTCTTATATACATATTTGGGCTTACAAATTCATCATCTATATTC 240
QY 241 TCCCTTCCGAGTCCCTTAAAGATTCATCCCTCAATCTTATTCCTCCCAATACGT 300
DB 241 TCCCTTCCGAGTCCCTTAAAGATTCATCCCTCAATCTTATTCCTCCCAATACGT 300
QY 301 TCTCTAATACAGTCTCTATATAGCAATACCTATATTTAGAGACATTTTTTATTTTGTAC 360
DB 301 TCTCTAATACAGTCTCTATATAGCAATACCTATATTTAGAGACATTTTTTATTTTGTAC 360
QY 361 ATACATATTTTGTCTATCTCTCAATGCAATATATCATATTTAGTTTACTTAAACCGATTAT 420
DB 361 ATACATATTTTGTCTATCTCTCAATGCAATATATCATATTTAGTTTACTTAAACCGATTAT 420
QY 421 TTTAAATATTTCAACGAGTGAAGAACTGTTTAAATTTCTATATATATAGAAATCCAGT 480
DB 421 TTTAAATATTTCAACGAGTGAAGAACTGTTTAAATTTCTATATATATAGAAATCCAGT 480
QY 481 AGCGTTCTCTAATTTAGATGATTTATTTAGAGAGCGCTGTTAGAAAACGTAAAAATTCG 540
DB 481 AGCGTTCTCTAATTTAGATGATTTATTTAGAGAGCGCTGTTAGAAAACGTAAAAATTCG 540
QY 541 TTGATTTATTTATATTTAGGTTAGAGTACCTTTATATCTTTATATGATCTTTGTGGACCA 600
DB 541 TTGATTTATTTATATTTAGGTTAGAGTACCTTTATATCTTTATATGATCTTTGTGGACCA 600
QY 601 GCGTTTACCGGTTATTTTCGGAATGGCGCTCTCATTTTCACCTCCAGGCCCCCAATTT 660
DB 601 GCGTTTACCGGTTATTTTCGGAATGGCGCTCTCATTTTCACCTCCAGGCCCCCAATTT 660
QY 661 TCACGTTTTTCAACGAGCGCCAGCGCTGCTTAACCAACAAATTTGTATCGGTGGCGGTT 720
DB 661 TCACGTTTTTCAACGAGCGCCAGCGCTGCTTAACCAACAAATTTGTATCGGTGGCGGTT 720
QY 721 TTCAAAAGAGTGGAAAACCATCTGACCCAGCACTAGTAGGCCCTCGGATCTCTCCG 780
DB 721 TTCAAAAGAGTGGAAAACCATCTGACCCAGCACTAGTAGGCCCTCGGATCTCTCCG 780
QY 781 ATTAAGTCTTAGGCATATAGAGCCCAACACCATCTAGCGGATGTGCTTACCGCTTC 840
DB 781 ATTAAGTCTTAGGCATATAGAGCCCAACACCATCTAGCGGATGTGCTTACCGCTTC 840
QY 841 CACCTCATGGGCGCGTCCATCTCCATCCAAACCTATTCGTTACCTTGCATCTCC 900
```

```
|||||
DB 841 CACCTCATGGGCGCGTCCATCTCCATCCAAACCTATTCGTTACCTTGCATCTCC 900
QY 901 GAAAAAATTTCTGGGTCCGCTCCGACCTACTCAATATACCATCCATCAACGAGAT 960
DB 901 GAAAAAATTTCTGGGTCCGCTCCGACCTACTCAATATACCATCCATCAACGAGAT 960
QY 961 CGCATCACTGCAATATCCCAAGAAATCAACACCTCCCAATTTCCACGCTGCACCACT 1020
DB 961 CGCATCACTGCAATATCCCAAGAAATCAACACCTCCCAATTTCCACGCTGCACCACT 1020
QY 1021 CGCGCTCTCCGCGCAAGACCAAGAAATTTGCGCCACCGCGGTGAGTCTCTCC 1080
DB 1021 CGCGCTCTCCGCGCAAGACCAAGAAATTTGCGCCACCGCGGTGAGTCTCTCC 1080
QY 1081 CCTCCCTCTCCGCGCGCGGTGACCAACCCCGCTCTCTCTTTCTTTCTCGGTTT 1140
DB 1081 CCTCCCTCTCCGCGCGCGGTGACCAACCCCGCTCTCTCTTTCTTTCTCGGTTT 1140
QY 1141 TTTTTCGTCGTGATCTGATCTTTGAGCTTTGAGTTGAGTGGGCGAGAGCGGCTTCG 1200
DB 1141 TTTTTCGTCGTGATCTGATCTTTGAGCTTTGAGTTGAGTGGGCGAGAGCGGCTTCG 1200
QY 1201 TCGCCCAAGTCGATCGCGGAGAGGCGGATCTCGCGGCTTGCGGCTTCGCGGCTGAGT 1260
DB 1201 TCGCCCAAGTCGATCGCGGAGAGGCGGATCTCGCGGCTTGCGGCTTCGCGGCTGAGT 1260
QY 1261 CGGCGCGGATCTCGCGGAGAGTGGGCTCTCGGATGATGATCTGATCGCGGCTTGG 1320
DB 1261 CGGCGCGGATCTCGCGGAGAGTGGGCTCTCGGATGATGATCTGATCGCGGCTTGG 1320
QY 1321 GGGAGATGATGGGCGGTTAAATTTCCCATGCTAAACAGATCAGAGAGGAGGAAAA 1380
DB 1321 GGGAGATGATGGGCGGTTAAATTTCCCATGCTAAACAGATCAGAGAGGAGGAAAA 1380
QY 1381 GGGCACTATGTTTATTTTATTTATTTTCTGCTGCTGCTGCTGCAAGCTTATGATGCT 1440
DB 1381 GGGCACTATGTTTATTTTATTTTATTTTCTGCTGCTGCTGCTGCTGCAAGCTTATGATGCT 1440
QY 1441 AGATCTTCTTCTCTTTTGTGGGTGAATTTGAATCCCTCAGCATTTGTTATCGGTA 1500
DB 1441 AGATCTTCTTCTCTTTTGTGGGTGAATTTGAATCCCTCAGCATTTGTTATCGGTA 1500
QY 1501 GTTTTCTTTTATGATTTGTGACAAATGACGCTCGTGCGGAGCTTTTGTAGTAGA 1560
DB 1501 GTTTTCTTTTATGATTTGTGACAAATGACGCTCGTGCGGAGCTTTTGTAGTAGA 1560
QY 1561 CCATG 1565
DB 1561 CCATG 1565

RESULT 2
US-10-758-799-3
; Sequence 3, Application US/10758799
; Publication No. US20040199944A1
; GENERAL INFORMATION:
; APPLICANT: DeRose, Richard
; Freysinet, Georges
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
; First Intron Of Rice Actin, Chimeric Gene Comprising It
; And Transformed Plant
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/758, 799
FILING DATE: 16-Jan-2004
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/037, 531
FILING DATE: 10-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: McMorrow Jr., Robert G.
REGISTRATION NUMBER: 30962
REFERENCE/DOCKET NUMBER: 5500+24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)658-9141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-758-799-3

Query Match 100.0%; Score 1565; DB 19; Length 1565;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCCTGAGGTCGAGCGATCCCTTATGTGACCACTTACTGTAATGCAATATCAT 60
DB 1 GAATTCCTGAGGTCGAGCGATCCCTTATGTGACCACTTACTGTAATGCAATATCAT 60
QY 61 TTAATGGAATGCAAACTTTCTATTACTCTTACTACATAATTCCTGTTTAAAT 120
DB 61 TTAATGGAATGCAAACTTTCTATTACTCTTACTACATAATTCCTGTTTAAAT 120
QY 121 TCAAGTCTCAACATTCATGCTCAAGTAAAGTTGAGACTGTCGAAATTTACTATTTAT 180
DB 121 TCAAGTCTCAACATTCATGCTCAAGTAAAGTTGAGACTGTCGAAATTTACTATTTAT 180
QY 181 TTCTTCATATTTTTCCTTATACATATTTGGGCTTACATCCATCTATATATCCA 240
DB 181 TTCTTCATATTTTTCCTTATACATATTTGGGCTTACATCCATCTATATATCCA 240
QY 241 TCCCTTCGGGTGCTCTTAAAGATTCATCTCTGAATCTTATTCCTCCAAATACGT 300
DB 241 TCCCTTCGGGTGCTCTTAAAGATTCATCTCTGAATCTTATTCCTCCAAATACGT 300
QY 301 TCTCTAATACAGTCTCTATPAGCAATCCTATATTAGAGACATTTTATTTTGTAC 360
DB 301 TCTCTAATACAGTCTCTATPAGCAATCCTATATTAGAGACATTTTATTTTGTAC 360
QY 361 ATATCATTTTGTCTATCTCAATGATATATATTTAGTTTACTTAAACGATAT 420
DB 361 ATATCATTTTGTCTATCTCAATGATATATATTTAGTTTACTTAAACGATAT 420
QY 421 TTAAGATTCAAACGATGAAAGCTGTTAGATAATCTATATATATAGAGATCCAGT 480
DB 421 TTAAGATTCAAACGATGAAAGCTGTTAGATAATCTATATATATAGAGATCCAGT 480
QY 481 AGCGTCTCTAATTTAGATGATTTATTAGAGACGCTGTAGAGAAACGTAAAAATCT 540
DB 481 AGCGTCTCTAATTTAGATGATTTATTAGAGACGCTGTAGAGAAACGTAAAAATCT 540
QY 541 TTGATTTATTTATTTAGGAGTAGAGCTTTATATGTTTATATATTTTGTGAGACCA 600
DB 541 TTGATTTATTTATTTAGGAGTAGAGCTTTATATGTTTATATATTTTGTGAGACCA 600
QY 601 GCCTTATACGGTATTTTGCAGATTCGCTCATTTTCACTCGACGCCACCATTT 660
DB 601 GCCTTATACGGTATTTTGCAGATTCGCTCATTTTCACTCGACGCCACCATTT 660

QY 661 TCAAGTTCACCGAAGCGCCAGCTGCTATACCAAAATTTGTACGGTGGCGGTT 720
DB 661 TCAAGTTCACCGAAGCGCCAGCTGCTTATACCAAAATTTGTACGGTGGCGGTT 720
QY 721 TTCAAAAGAAATCGAAGCAATCTGACCCAGCACTAGTAGGCGCTCGATCTCCCT 780
DB 721 TTCAAAAGAAATCGAAGCAATCTGACCCAGCACTAGTAGGCGCTCGATCTCCCT 780
QY 781 ATTTAAGTCTTACCAATTTAGAGCCGCAACCACTTACAGCGGATTCCTTACGTTCC 840
DB 781 ATTTAAGTCTTACCAATTTAGAGCCGCAACCACTTACAGCGGATTCCTTACGTTCC 840
QY 841 CACCTATCGGCGCGCTGCAATCTTCAACCACTATTCCTTACCTTCCATCCATCC 900
DB 841 CACCTATCGGCGCGCTGCAATCTTCAACCACTATTCCTTACCTTCCATCCATCC 900
QY 901 GAAAAAATTCCTCGGCTCGGCTCCGACCTACTACAAATATCCATCCATCCATCC 960
DB 901 GAAAAAATTCCTCGGCTCGGCTCCGACCTACTACAAATATCCATCCATCCATCC 960
QY 961 CGCATCACTGCAAAATCCCGAAGAAATCAACCTCCCAATTCACGCTGCCACCACT 1020
DB 961 CGCATCACTGCAAAATCCCGAAGAAATCAACCTCCCAATTCACGCTGCCACCACT 1020
QY 1021 CGCGCTCTCCGCGCAAGACCAAGAAATTTGGCCGACCGCGGTGAGCTCTCC 1080
DB 1021 CGCGCTCTCCGCGCAAGACCAAGAAATTTGGCCGACCGCGGTGAGCTCTCC 1080
QY 1081 CTTCCCTCTCCGCGCGCAAGACCAAGAAATTTGGCCGACCGCGGTGAGCTCTCC 1140
DB 1081 CTTCCCTCTCCGCGCGCAAGACCAAGAAATTTGGCCGACCGCGGTGAGCTCTCC 1140
QY 1141 TTTTTCCTCTCGGCTCGAATCTTGTGAGCTTGTGAGGCTGAGGCGAGGCTTCC 1200
DB 1141 TTTTTCCTCTCGGCTCGAATCTTGTGAGCTTGTGAGGCTGAGGCGAGGCTTCC 1200
QY 1201 TCGCCCAAGATCGGTGCGCGGAGAGGCGGATCTCGCGCTGCGGCTCTCCGCGCTGAGT 1260
DB 1201 TCGCCCAAGATCGGTGCGCGGAGAGGCGGATCTCGCGCTGCGGCTCTCCGCGCTGAGT 1260
QY 1261 CGGCGCGGATCCCTCGCGGGAATGAGGAGCTCTCGGATGATCTGATCCGCGTGTGG 1320
DB 1261 CGGCGCGGATCCCTCGCGGGAATGAGGAGCTCTCGGATGATCTGATCCGCGTGTGG 1320
QY 1321 GGGAGATGATGAGGCGCTTAAATTTTCCCATGCTTAAACAGATCGAAGAGGGGAAA 1380
DB 1321 GGGAGATGATGAGGCGCTTAAATTTTCCCATGCTTAAACAGATCGAAGAGGGGAAA 1380
QY 1381 GGGACATATGTTTATATTTTATATATTTCTGCTGCTGCTCAAGGCTTATATGCT 1440
DB 1381 GGGACATATGTTTATATTTTATATATTTCTGCTGCTGCTCAAGGCTTATATGCT 1440
QY 1441 AGATCTTCTCTCTCTTCTTCTTGTGAGGATGAAATTTGAATCCCTGAGATTTTATCGGTA 1500
DB 1441 AGATCTTCTCTCTCTTCTTCTTGTGAGGATGAAATTTGAATCCCTGAGATTTTATCGGTA 1500
QY 1501 GTTTTCTTTTCAATGATTTGTGCAAAATGAGGCTGTGTGAGAGCTTTTGTAGGTAGA 1560
DB 1501 GTTTTCTTTTCAATGATTTGTGCAAAATGAGGCTGTGTGAGAGCTTTTGTAGGTAGA 1560
QY 1561 CCATG 1565
DB 1561 CCATG 1565

RESULT 3
US-09-037-531-1
; Sequence 1, Application US/09037531
; Patent No. US20020104117A1
; GENERAL INFORMATION:
; APPLICANT: DeRose, Richard
; APPLICANT: Freytsinet, Georges
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The

TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
TITLE OF INVENTION: And Transformed Plant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,531
FILING DATE: 10-MAR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McMorrow Jr., Robert G.
REGISTRATION NUMBER: 30962
REFERENCE/DOCKET NUMBER: 5500*24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)658-9141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1021 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-037-531-1

Query Match 65.2%; Score 1021; DB 9; Length 1021;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 CTTATGTGACCCCTTAACTGTAATGATATCATATTAATGATAGAACTTTCTATT 86
1 CTTATGTGACCCCTTAACTGTAATGATATTAATGATAGAACTTTCTATT 60
87 ACTCTTTTACTAATATCTGTTTAAATTCAGTCTCAACATTCATTCCTCAAG 146
61 ACTCTTTTACTAATATCTGTTTAAATTCAGTCTCAACATTCATTCCTCAAG 120
147 TATAGTGTGAGCTGTCAAAATTTACTATTTTATTTCTCATATTTTTCCTTAA 206
121 TATAGTGTGAGCTGTCAAAATTTACTATTTTATTTCTCATATTTTTCCTTAA 180
207 CATTTTGGGCTTACATCATCATATTCATCTTCCTGCTGCTCTTAAAGATT 266
181 CATTTTGGGCTTACATCATCATATTCATCTTCCTGCTGCTCTTAAAGATT 240
267 CCATCCCTGATCTTATCTCTCCCATATAGCTTCTTAATCAGGCTCTTAAAGCAA 326
241 CCATCCCTGATCTTATCTCTCCCATATAGCTTCTTAAACAGGCTCTTAAAGCAA 300
327 TACCTATATTAGAGACATTTTATTTTGTACATACATATTTGTCAATCTCAATG 386
301 TACCTATATTAGAGACATTTTATTTTGTACATACATATTTGTCAATCTCAATG 360
387 CATTATACATATTAGTTTACTTAAACCGATTTATTTAAATTTTCAACGAGTGAAGAC 446
361 CATTATACATATTAGTTTACTTAAACCGATTTATTTAAATTTTCAACGAGTGAAGAC 420
447 TGTTTAGATAAATTTCTATATATAGAGATCAAGTAGGCTCTCAATTTAGATGATAT 506
421 TGTTTAGATAAATTTCTATATATAGAGATCAAGTAGGCTCTCAATTTAGATGATAT 480
507 TTAGAGAGCGCTGTAGAGAAACGTAAATTTCTTTGATTATTTATTTAGGTAGAGT 566
481 TTAGAGAGCGCTGTAGAGAAACGTAAATTTCTTTGATTATTTATTTAGGTAGAGT 540

567 ACCCTTTAGCTTTATAGATCTTTGTGAGACCCAGCTTAATCCGGTATTTTCCGAT 626
541 ACCCTTTAGCTTTATAGATCTTTGTGAGACCCAGCTTAATCCGGTATTTTCCGAT 600
627 GGGCTCTCATTTTCACTTCAGCGCCCAATTTTACGTTTCAACCGAGGCCAGCC 686
601 GGGCTCTCATTTTCACTTCAGCGCCCAATTTTACGTTTCAACCGAGGCCAGCC 660
687 TGCCTAACCAAAATTTGTAGGAGCGCGGCTTTTCAAAAGAGTGGAAACCATCTGC 746
661 TGCCTAACCAAAATTTGTAGGAGCGCGGCTTTTCAAAAGAGTGGAAACCATCTGC 720
747 ACCCAACGACTGTAGGAGCGCGCTGATTCCTCCCTGATTAAGTCTCAATAGAGCCCA 806
721 ACCCAACGACTGTAGGAGCGCGCTGATTCCTCCCTGATTAAGTCTCAATAGAGCCCA 780
807 GAACCAACCATCAGCGGATCGTCCCTAAGCTTCACTCATGAGCGCGCTCATCTCCA 866
781 GAACCAACCATCAGCGGATCGTCCCTAAGCTTCACTCATGAGCGCGCTCATCTCCA 840
867 TCCACACCTATTCGGTAACTTGCACATCTCCGAAATTTCTCGGCTCGCGCTCGC 926
841 TCCACACCTATTCGGTAACTTGCACATCTCCGAAATTTCTCGGCTCGCGCTCGC 900
927 ACTTACTACAAATACCATCCATCCATCAGCAGCATGCAATCTGCAATCCCGAGAA 986
901 ACTTACTACAAATACCATCCATCCATCAGCAGCATGCAATCTGCAATCCCGAGAA 960
987 ATCAACACCTCCCAATTTCCAGCTGCGCAACAACTGCGGCTCTCGCGCGCAACAA 1046
961 ATCAACACCTCCCAATTTCCAGCTGCGCAACAACTGCGGCTCTCGCGCGCAACAA 1020

1047 G 1047
1021 G 1021

RESULT 4
US-10-758-799-1
Sequence 1, Application US/10758799
Publication No. US2004019944A1
GENERAL INFORMATION:
APPLICANT: Derose, Richard
TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
First Intron Of Rice Actin, Chimeric Gene Comprising It
And Transformed Plant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/758,799
FILING DATE: 16-Jan-2004
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/037,531
FILING DATE: 10-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: McMorrow Jr., Robert G.
REGISTRATION NUMBER: 30962
REFERENCE/DOCKET NUMBER: 5500*24
TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 658-9141
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1021 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-758-799-1

Query Match 65.2%; Score 1021; DB 19; Length 1021;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1021; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 27 CTTATGTGACCACTTATCTGTAAATGCAATATCAATTTATGAATAGCAAACTTTCTATT 86
DB 1 CTTATGTGACCACTTATCTGTAAATGCAATATCAATTTATGAATAGCAAACTTTCTATT 60
QY 87 ACTTCTTTACTAATATATCTGTTTAAATTCAGTCTCTCAACTTATTGCTCAAG 146
DB 61 ACTTCTTTACTAATATCTGTTTAAATTCAGTCTCTCAACTTATTGCTCAAG 120
QY 147 TATAGTTGAGACGTGCAAAATTTACTATTTTCTGATATTTTCTTATGATAC 206
DB 121 TATAGTTGAGACGTGCAAAATTTACTATTTTCTGATATTTTCTTATGATAC 180
QY 207 CATTTTGGGCTTACATCCATCATCTATATCCATCTTTCGGTGTCTCTAAAGATT 266
DB 181 CATTTTGGGCTTACATCCATCATCTATATCCATCTTTCGGTGTCTCTAAAGATT 240
QY 267 CCATCTCTGATCTTATCTCTCCCAATACGTTCTTAAATCAGTCTCTAATGCAA 326
DB 241 CCATCTCTGATCTTATCTCTCCCAATACGTTCTTAAATCAGTCTCTAATGCAA 300
QY 327 TACCTATATAGAGACATTTTATTTTGTGACATCATATTTGATCTCTCAATG 386
DB 301 TACCTATATAGAGACATTTTATTTTGTGACATCATATTTGATCTCTCAATG 360
QY 387 CATTATCATATTTAGTTTACTTAAACCGATTTATTTAAATTCATCAACGATGAAAC 446
DB 361 CATTATCATATTTAGTTTACTTAAACCGATTTATTTAAATTCATCAACGATGAAAC 420
QY 447 TGTTTAGATAAATCTATATATAGAGATCCAGTGGTCTCTAAATTTAGATGATT 506
DB 421 TGTTTAGATAAATCTATATATAGAGATCCAGTGGTCTCTAAATTTAGATGATT 480
QY 507 TTGAGAGACGCTGTAGAAAAAGTAAAAATTTCTTGATTTATTTATTTAGGTAGAGT 566
DB 481 TTGAGAGACGCTGTAGAAAAAGTAAAAATTTCTTGATTTATTTATTTAGGTAGAGT 540
QY 567 AGCTTTATGCTTATATGATCTTTGTGAGACCGACCTTATACCGGTTATTTTCGAGAT 626
DB 541 AGCTTTATGCTTATATGATCTTTGTGAGACCGACCTTATACCGGTTATTTTCGAGAT 600
QY 627 GCGCCTCTCAATTTCACTCCAGCGCCCAATTTTCAAGTTTTCACCGAAGCGCCAGCC 686
DB 601 GCGCCTCTCAATTTCACTCCAGCGCCCAATTTTCAAGTTTTCACCGAAGCGCCAGCC 660
QY 687 TGCTTAACCAAAATTTGTAGCGGTGGCGGTTTCAAAAGAGTGGAAACCATTTGCG 746
DB 661 TGCTTAACCAAAATTTGTAGCGGTGGCGGTTTCAAAAGAGTGGAAACCATTTGCG 720
QY 747 ACCCAGCAGTATAGAGCCCTCGGATCTCTCGATTAAGTCTAGGCAATAGAGAGCCA 806
DB 721 ACCCAGCAGTATAGAGCCCTCGGATCTCTCGATTAAGTCTAGGCAATAGAGAGCCA 780
QY 807 GAACCACTCATACGCGGATGTCCTTAACGCTTCACTCATGCGCGCGCTCATCTCCA 866
DB 781 GAACCACTCATACGCGGATGTCCTTAACGCTTCACTCATGCGCGCGCTCATCTCCA 840
QY 867 TCGAAGCCTATTCGTTACCTTGGCCATCTCCGAAAAAATTTCTGGGCTCGGCTCGCG 926
  
```

```

DB 841 TCGAAGCCTATTCGTTACTCTTGGCCATCTCTCCGAAAAAATTTCTGGCTCGGCTCGCG 900
QY 927 ACCTACTACAAATATCCATATCCATATCCATATCCATATCCATATCCATATCCATATCC 986
DB 901 ACCTACTACAAATATCCATATCCATATCCATATCCATATCCATATCCATATCCATATCC 960
QY 987 ATCAACACTCTCCCAATTTCCAGCGTGCACCAACTGCGCTCTCGCGCAAGCAACAA 1046
DB 961 ATCAACACTCTCCCAATTTCCAGCGTGCACCAACTGCGCTCTCGCGCAAGCAACAA 1020
QY 1047 G 1047
DB 1021 G 1021
  
```

```

RESULT 5
US-09-037-531-2
; Sequence 2, Application US/09037531
; Patent No. US20020104117A1
; GENERAL INFORMATION:
; APPLICANT: Derose, Richard
; TITLE OF INVENTION: Freysinet, Georges
; TITLE OF INVENTION: Maize H3C4 Promoter Combined With The
; TITLE OF INVENTION: First Intron Of Rice Actin, Chimeric Gene Comprising It
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,531
; FILING DATE: 10-MAR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G.
; REGISTRATION NUMBER: 30962
; REFERENCE/DOCKET NUMBER: 5500*24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-037-531-2
  
```

Query Match 29.0%; Score 454; DB 9; Length 454;
 Best Local Similarity 100.0%; Pred. No. 3.8e-219;
 Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1102 GTAAACACCCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1161
DB 1 GTAAACACCCCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
QY 1162 CTTTGGCTTTGGATGTTTGGGTGGGAGAGGCGGCTTGGCGCCAGATCGGTCGCGAT 1221
DB 61 CTTTGGCTTTGGATGTTTGGGTGGGAGAGGCGGCTTGGCGCCAGATCGGTCGCGAT 120
QY 1222 AGGGGCGGAGATCTCGCGGCTGGGCTCTCGGCGGTGAGTTCGCGCGCGGATCTTCGCGG 1281
DB 121 AGGGGCGGAGATCTCGCGGCTGGGCTCTCGGCGGTGAGTTCGCGCGCGGATCTTCGCGG 180
  
```



```

Db      4603 CCGGGCGTGAATCGGCGCCGGATCTCGCGGGGAAATCGGGCTCTCGATGTAAATCT 4658

RESULT 11
US-09-991-209-34
; Sequence 34, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 4950
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pJ06.1 vector
US-09-991-209-34

Query Match      15.1%; Score 236; DB 10; Length 4950;
Best Local Similarity 100.0%; Pred. No. 1.5e-108; Mismatches 0; Indels 0; Gaps 0;
Matches 236; Conservative 0;

Db      1069 GAGCTCTCTCCCTCCCTCCGCGCGCGGGTAAACACCCGCGCTCTCTTTC 1128
4600 GAGCTCTCTCCCTCCCTCCGCGCGCGGGTAAACACCCGCGCTCTCTTTC 4659

Qy      1129 TTTCTCCGTTTTTTTTTTCGTCCTCGATCTTTCGCTTGTAGTTGGGTGGCG 1188
4660 TTTCTCCGTTTTTTTTTTCGTCCTCGATCTTTCGCTTGTAGTTGGGTGGCG 4719

Db      1189 AGAGGGGCTTCCTCCCGCAGATCGGTGGCGGGGAGGGAGATCTCGGGCTGGGCTCT 1248
4720 AGAGGGGCTTCCTCCCGCAGATCGGTGGCGGGGAGGGAGATCTCGGGCTGGGCTCT 4779

Qy      1249 CCGGGCGTGAATCGGCGCCGGATCTCTCGCGGGAATGGGCTCTCGATGTAAATCT 1304
4780 CCGGGCGTGAATCGGCGCCGGATCTCTCGCGGGAATGGGCTCTCGATGTAAATCT 4835

RESULT 12
US-09-991-209-37
; Sequence 37, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 4965
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

```

; OTHER INFORMATION: pJ03 vector
US-09-991-209-37

Query Match          15.1%; Score 236; DB 10; Length 4965;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1069 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGCGCGGATCAACACCCGCGCCCTCTCTCTTTC 1128
DB      504 GAGCTCTCTCCCTCCCTCCCTCCCTCCGCGCGCGCGGATCAACACCCGCGCCCTCTCTCTTTC 563

QY      1129 TTCTCCGTTTTTTTTTTCGTGCTCGATCTCGATCTTGGCTTGGATGGAGCG 1188
DB      564 TTCTCCGTTTTTTTTTTCGTGCTCGATCTCGATCTTGGCTTGGATGGAGCG 623

QY      1189 AGAGCGGCTTTCGTGCGCCAGATCGGTGCGCGAGAGAGCGCGGATCTCGCGCTGCGCTT 1248
DB      624 AGAGCGGCTTTCGTGCGCCAGATCGGTGCGCGAGAGAGCGCGGATCTCGCGCTGCGCTT 683

QY      1249 CCGGCGGTGAGTCGCGCCGAGATCTTCGCGGGGGAATGGGAGCTCTCGATGTAGATCT 1304
DB      684 CCGGCGGTGAGTCGCGCCGAGATCTTCGCGGGGGAATGGGAGCTCTCGATGTAGATCT 739

RESULT 13
US-09-991-209-35
; Sequence 35; Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OR INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ. ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 4974
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: pJ04 vector
US-09-991-209-35

Query Match          15.1%; Score 236; DB 10; Length 4974;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1069 GAGCTCTCTCCCTCTCCCTCTCGCGCGCGCGCGGATCAACACCCGCGCCCTCTCTTTC 1128
DB      504 GAGCTCTCTCCCTCTCCCTCTCCCTCTCGCGCGCGCGGATCAACACCCGCGCCCTCTCTTTC 563

QY      1129 TTCTCCGTTTTTTTTTTCGTGCTCGATCTTGGCTTGGATGGAGCG 1188
DB      564 TTCTCCGTTTTTTTTTTCGTGCTCGATCTTGGCTTGGATGGAGCG 623

QY      1189 AGAGCGGCTTTCGTGCGCCAGATCGGTGCGCGAGAGAGCGCGGATCTCGCGCTGCGCTT 1248
DB      624 AGAGCGGCTTTCGTGCGCCAGATCGGTGCGCGAGAGAGCGCGGATCTCGCGCTGCGCTT 683

QY      1249 CCGGCGGTGAGTCGCGCCGAGATCTTCGCGGGGGAATGGGAGCTCTCGATGTAGATCT 1304
DB      684 CCGGCGGTGAGTCGCGCCGAGATCTTCGCGGGGGAATGGGAGCTCTCGATGTAGATCT 739

RESULT 14
US-09-991-209-36

```



```
; Sequence 36, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 5164
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pPO10.1 vector
US-09-991-209-36
```

```
Query Match      15.1%; Score 236; DB 10; Length 5164;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1069 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCCGCCCTCTCTCTTTTC 1128
    |||||
DB 4814 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCCGCCCTCTCTCTTTTC 4873

QY 1129 TTCTCCGTTTTTTTTTTTGTCTCGATCTTGACCTTTGGATTGGGTGGCG 1188
    |||||
DB 4874 TTCTCCGTTTTTTTTTTTGTCTCGATCTTGACCTTTGGATTGGGTGGCG 4933

QY 1189 AGAGCGGCTTCTGTCGCCCAAGTCGTGCGGAGGCGCGGATCTCGCGCTGGCGTCT 1248
    |||||
DB 4934 AGAGCGGCTTCTGTCGCCCAAGTCGTGCGGAGGCGCGGATCTCGCGCTGGCGTCT 4993

QY 1249 CCGGCGGTGAGTCGCGCGCGGATCTCGCGGAGATGGGGCTCTCGATGTAGATCT 1304
    |||||
DB 4994 CCGGCGGTGAGTCGCGCGCGGATCTCGCGGAGATGGGGCTCTCGATGTAGATCT 5049
```

RESULT 15

```
US-09-991-209-25
; Sequence 25, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 5277
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTP5-1 vector
US-09-991-209-25
```

```
Query Match      15.1%; Score 236; DB 10; Length 5277;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
```

```
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1069 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCCGCCCTCTCTTTTC 1128
    |||||
DB 4930 GAGCTCTCTCCCTCCCTCCCTCCGCGCGCGGTAAACACCCCGCCCTCTCTTTTC 4989

QY 1129 TTCTCCGTTTTTTTTTTTGTCTCGATCTTGACCTTTGGATTGGGTGGCG 1188
    |||||
DB 4990 TTCTCCGTTTTTTTTTTTGTCTCGATCTTGACCTTTGGATTGGGTGGCG 5049

QY 1189 AGAGCGGCTTCTGTCGCCCAAGTCGTGCGGAGGCGCGGATCTCGCGCTGGCGTCT 1248
    |||||
DB 5050 AGAGCGGCTTCTGTCGCCCAAGTCGTGCGGAGGCGCGGATCTCGCGCTGGCGTCT 5109

QY 1249 CCGGCGGTGAGTCGCGCGCGGATCTCGCGGAGATGGGGCTCTCGATGTAGATCT 1304
    |||||
DB 5110 CCGGCGGTGAGTCGCGCGCGGATCTCGCGGAGATGGGGCTCTCGATGTAGATCT 5165
```

```
Search completed: September 12, 2005, 16:58:30
Job time : 831.171 secs
```

THIS PAGE BLANK (USPTO)